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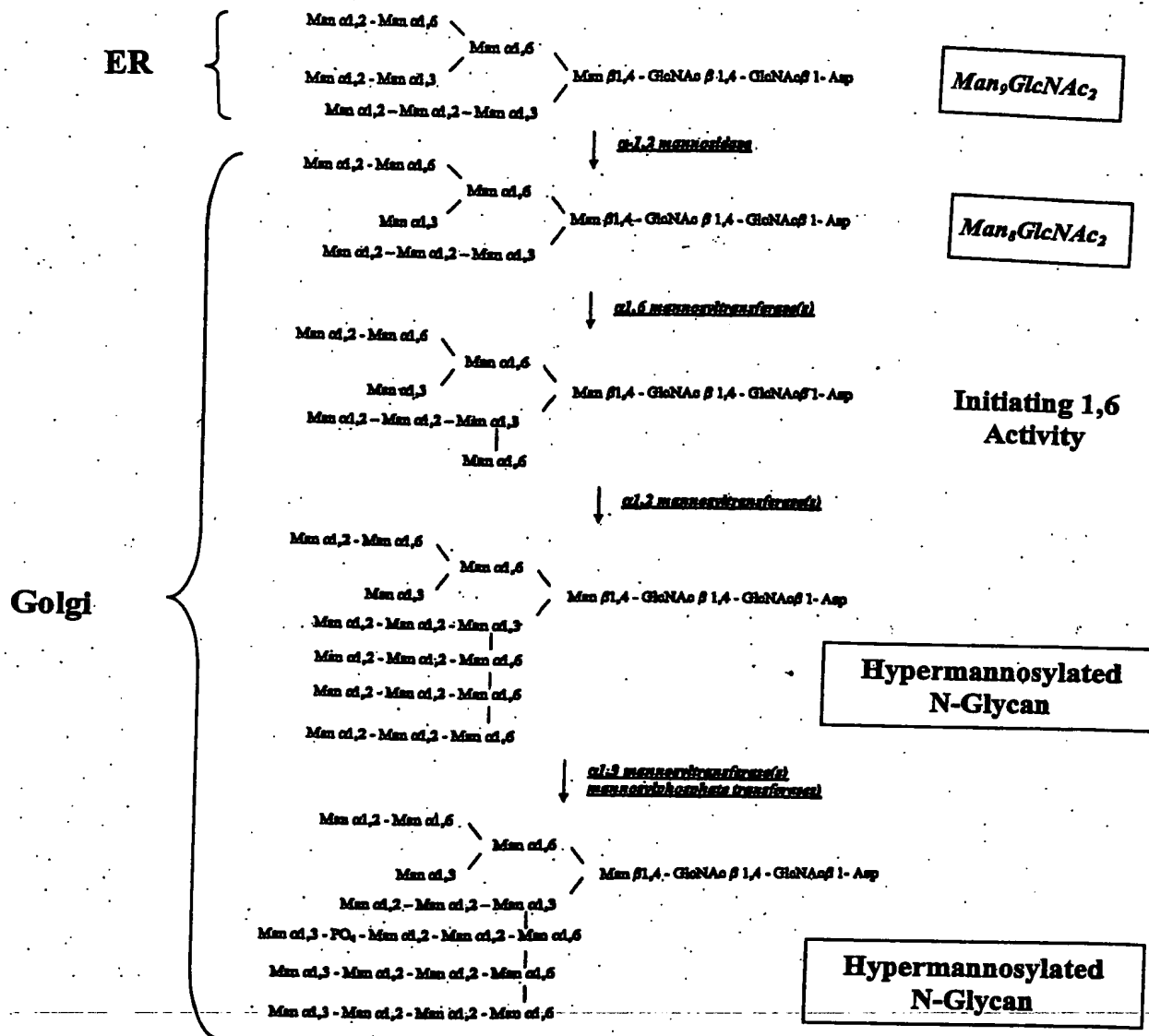


Fig. 1A

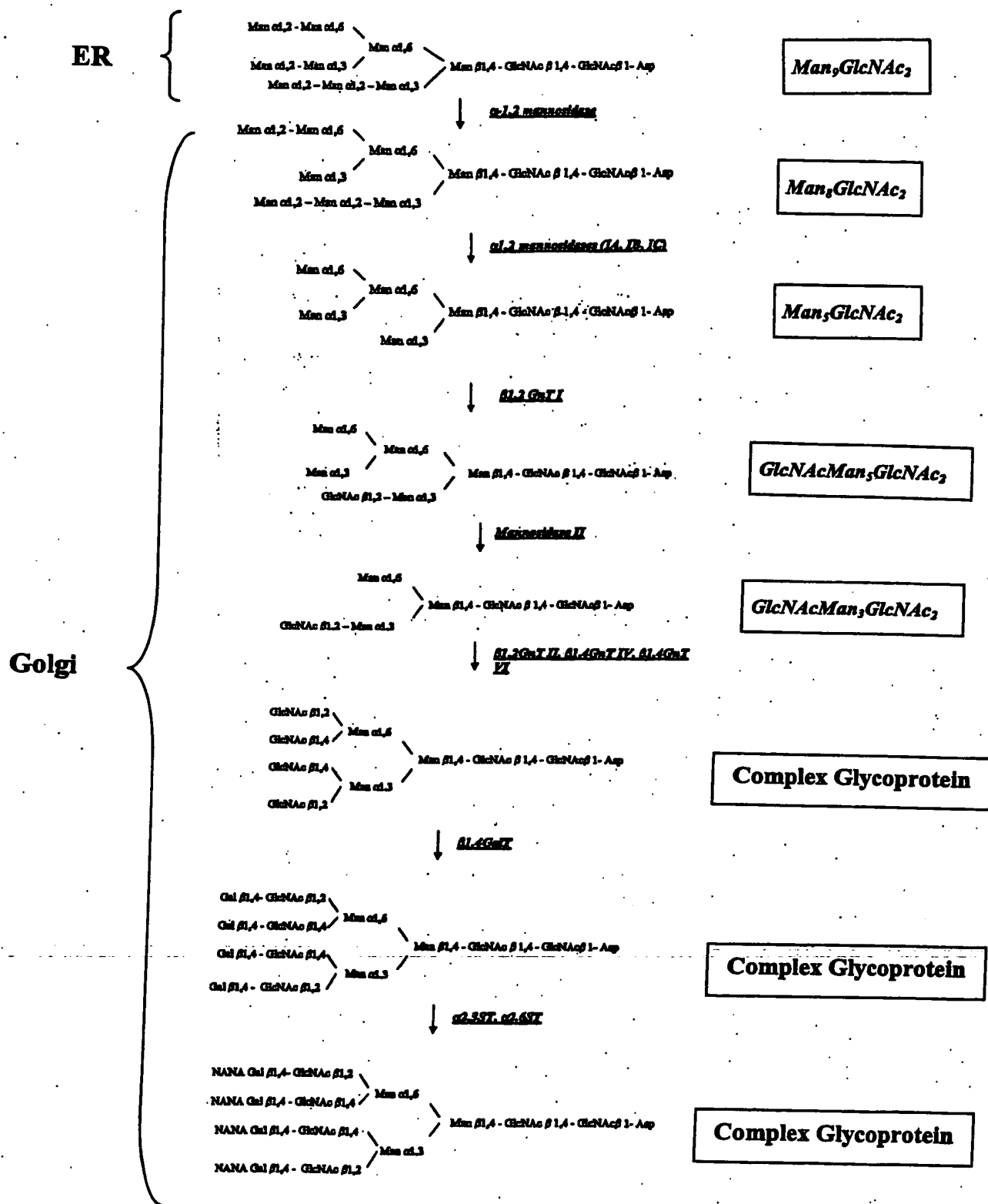


Fig. 1B

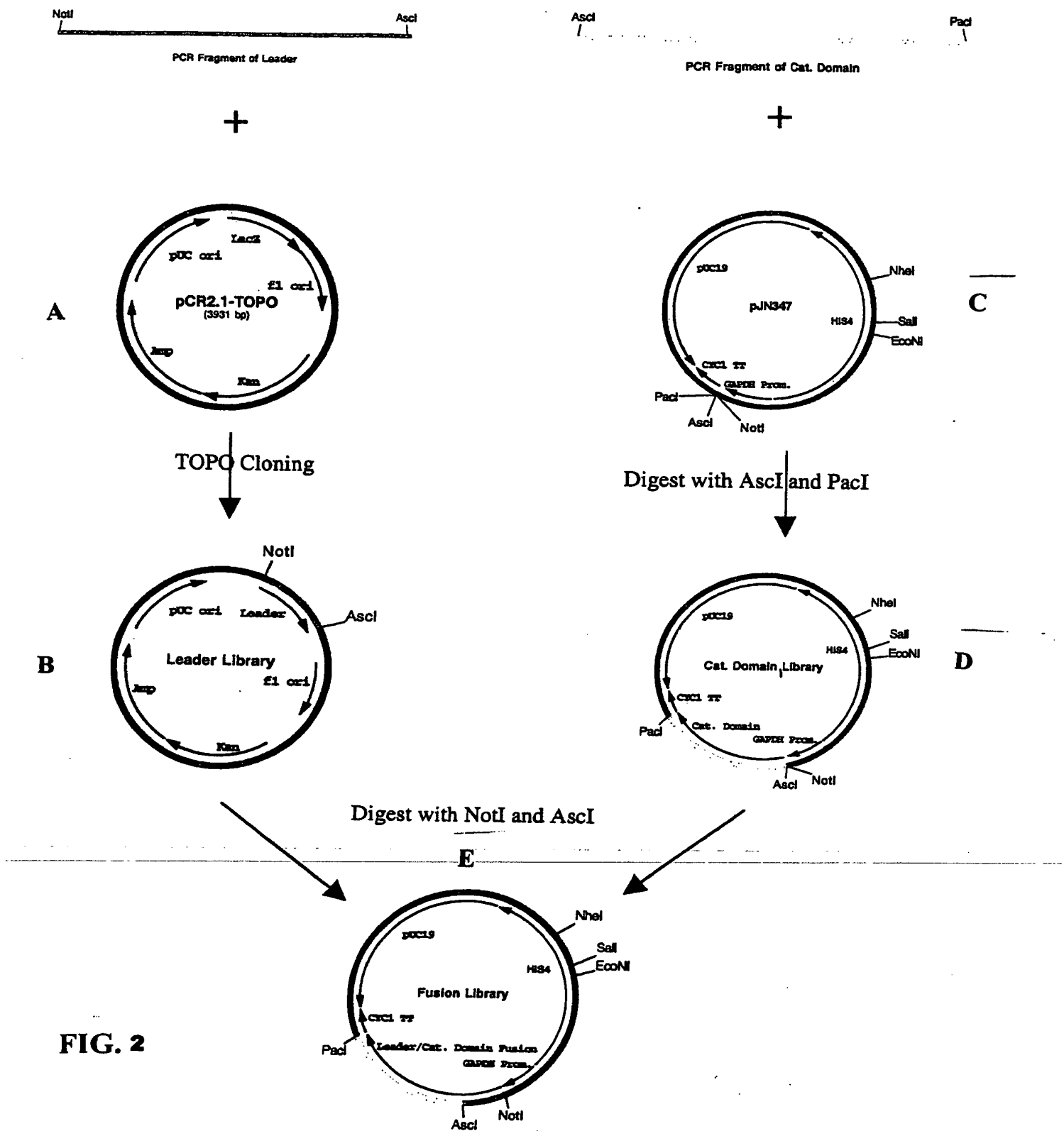


FIG. 2

FIG. 3

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

```
1 atgcccgtgggggctgttgcgcctcttcagtagccctggggggcgccgctggcagtgccctgggcggggggcttggcgggcgaggagggg
1▶ M P V G G L L P L F S S P G G G G L G S G L G G G L G G G R K G
97 tctggccccgtgccttccgctccaccgagaagtctgtgctgctgctggtgttcagcgcccttcacacgctctgtcttggggcaatc
33▶ S G P A A F R L T E K F V L L L V F S A F I T L C F G A I
184 tcttctctgcttgaatctctccagctgctcaggggctctgcttccactcccaacctgcttgcagcccgccggcgagcacaagcccggtctg
62▶ F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L
d65 primer
278 gggcgctgcggaggatgcgcgcgggggagagtcgggcccgcgagggagggcgccctgggggaccccgaggctgggactggaagacaacttagcca
93▶ G A R A E D A A E G R V R H R E E G A P G D P G A G L E D N L A
d105 primer
374 ggatccgcgaaaccacgagcggtctctcagggagccaaggagacctgcagaagctgcggaggagatccaaagagacattctgctggagaagg
125▶ R I R E N H E R A L R E A K E T L Q K L P E E I Q R D I L L E K
470 aaaaggtggcccgagaccagctgcgtgacaaggatctgttttaggggcttgcaccaagggtggacttctgcccccgctcggggtagagaaccgggagc
157▶ E K V A Q D Q L R D K D L F R G L P K V D F L P P V G V E N R E
d187 primer
566 ccgctgacgccaccatccgtggaagaggggcaagatcaaaagagatgatgacccatgcttggaaataattataaacgctatcgctggggc
189▶ P A D A T I R E K R A K I K E M M T H A W N N Y K R Y A W G
655 ttgaacgaactgaacctatatcaaaaagaaggccattcaagcagtttctgttggcaacatcaaaaggagctacaatagtagatg
219▶ L N E L K P I S K E G H S S S L F G N I K G A T I V D
737 ccttggatacccttttcttattatgggcatgaagactgaatttcaagaagctaaatcgtggattaaaaaatatttagattttan
246▶ A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N
819 tctgaatgctgaagttctgttcttttgaagtcacatagcttctgtctggactgctgtcagcctactatttgcggagag
273▶ V N A E V S V F E V N I R F V G G L L S A Y Y L S G E
901 gagatatttccgaagaagcagtggaacttggggtaaaattgctacctgcatcttatactccctctggaatcccttgggcat
302▶ E I F R K K A V E L G V K L L P A F H T P S G I P W A
983 tctgtaatatgaagaatgggagtcggggcggaactggcccttgggctctggaggcagcagtatccctggccgaatttgggaactct
328▶ L L N M K S G I G R N W P W A S G G S S I L A E F G T L
1065 gcattttagagtttatgcaacttgtcccacttatcaggagagaccagctcttggcgaaaagggttatgaaattcgaacagtggtg
355▶ H L E F M H L S H L S G D P V F A E K V M K I R T V L
1147 acaaaactggacaaaccagaggcctttatcctaactatctgaacccagtagtgagcagtggttgcacacatcatgtgtctgg
383▶ N K L D K P E G L Y P N Y L N P S S G Q W G Q H H V S
1229 ctggaggacttgggagacagcttttatgaatatttgccttaaggcggtggttaattgtctgacaagacagatctcgaagcnaagaa
410▶ V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K
1311 gatgtattttgatgctgttccagccatcgagactcacttgatccgcaagtcgaagtggggactaacgtacatcgcagagtg
437▶ M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W
1393 aaggggggctcctctggaaacacaaagatggggccacctgacgtgcttggcaggaggcatgtttgcaacttggggcagatggagctc
465▶ K G G L L E H K M G H L T C F A G G M F A L G A D G A
1475 cggaaagcccgggcccaactaccttgaactcggagctgaatttggccgcaacttgcataatcttataatcgtacatatgt
492▶ P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V
1557 gaagtgggaccgggaagcgttttgcatttgcgggtgtgggaagctatttggccagaggcaaatgaaaagtattacatctta
519▶ K L G P E A F R F D G V E A I A T R Q N E K Y Y I L
1639 cgcccgaggtctcagagacatacatgtacatgtgtgcgactgactcacgaccccaagtacaggacctggggcctgggaagccg
547▶ R P E V I E T Y M Y M W R L T H D P K Y R T W A W E A
1721 tggaggctctagaagaatcactgcagagtgaaacggaggctactcaggcttaccgggatgtttacatttggccgtgagagttatga
574▶ V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D
1803 cgatgtccagcaagttcttcttctggcagagacactgaagtatttgccttacttgatatttccgatgatgaccttcttccacta
601▶ D V Q Q S F F L A E T L K Y L I F S D D D L L P L
1885 gaacactggatottcaacacggaggtctatccttccctatactccgtgaacagaagaggaaattgatggcaagagaaatga
629▶ E H W I F N T E A H P F P I L R E Q K K E I D G K E K
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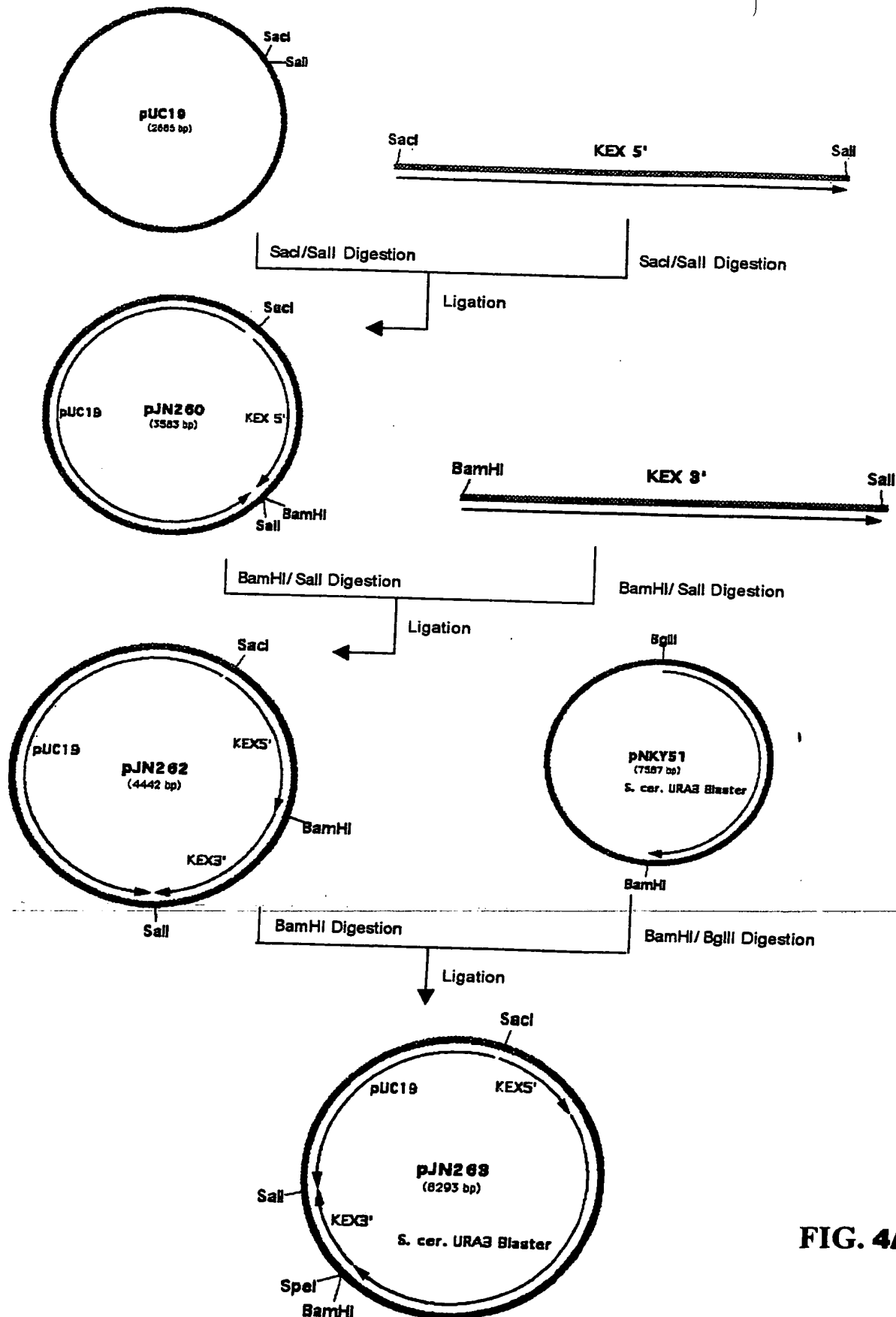


FIG. 4A

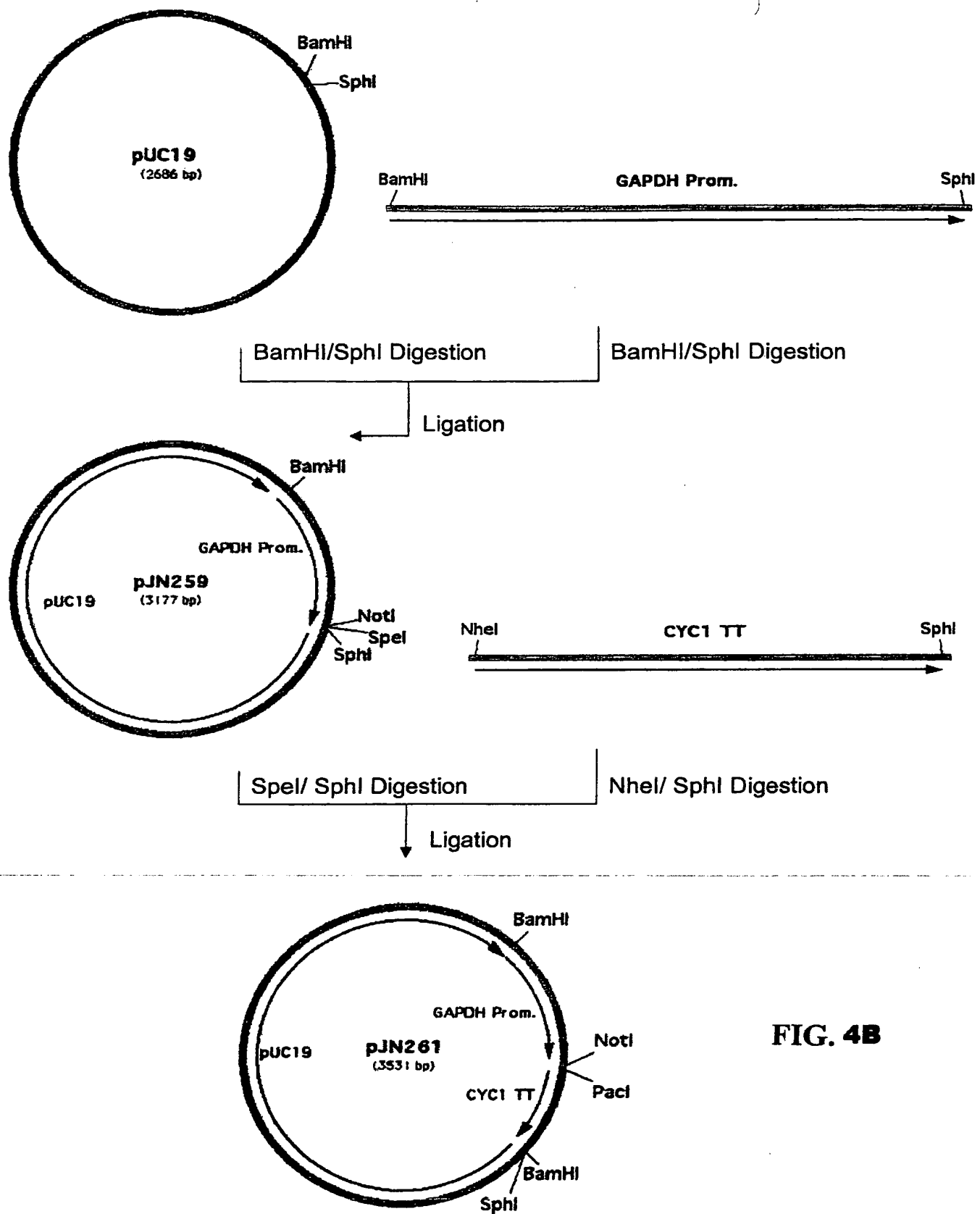


FIG. 4B

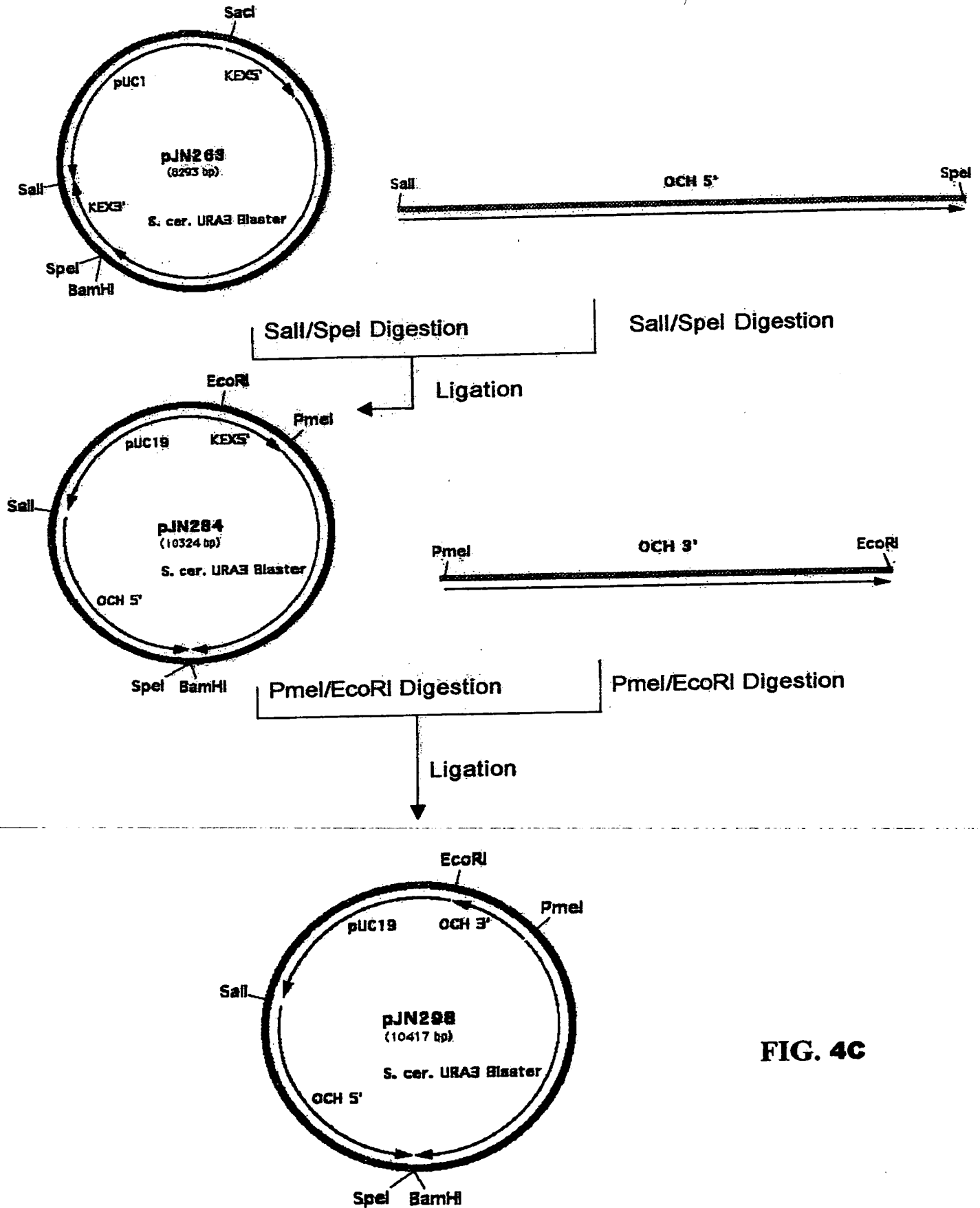


FIG. 4C

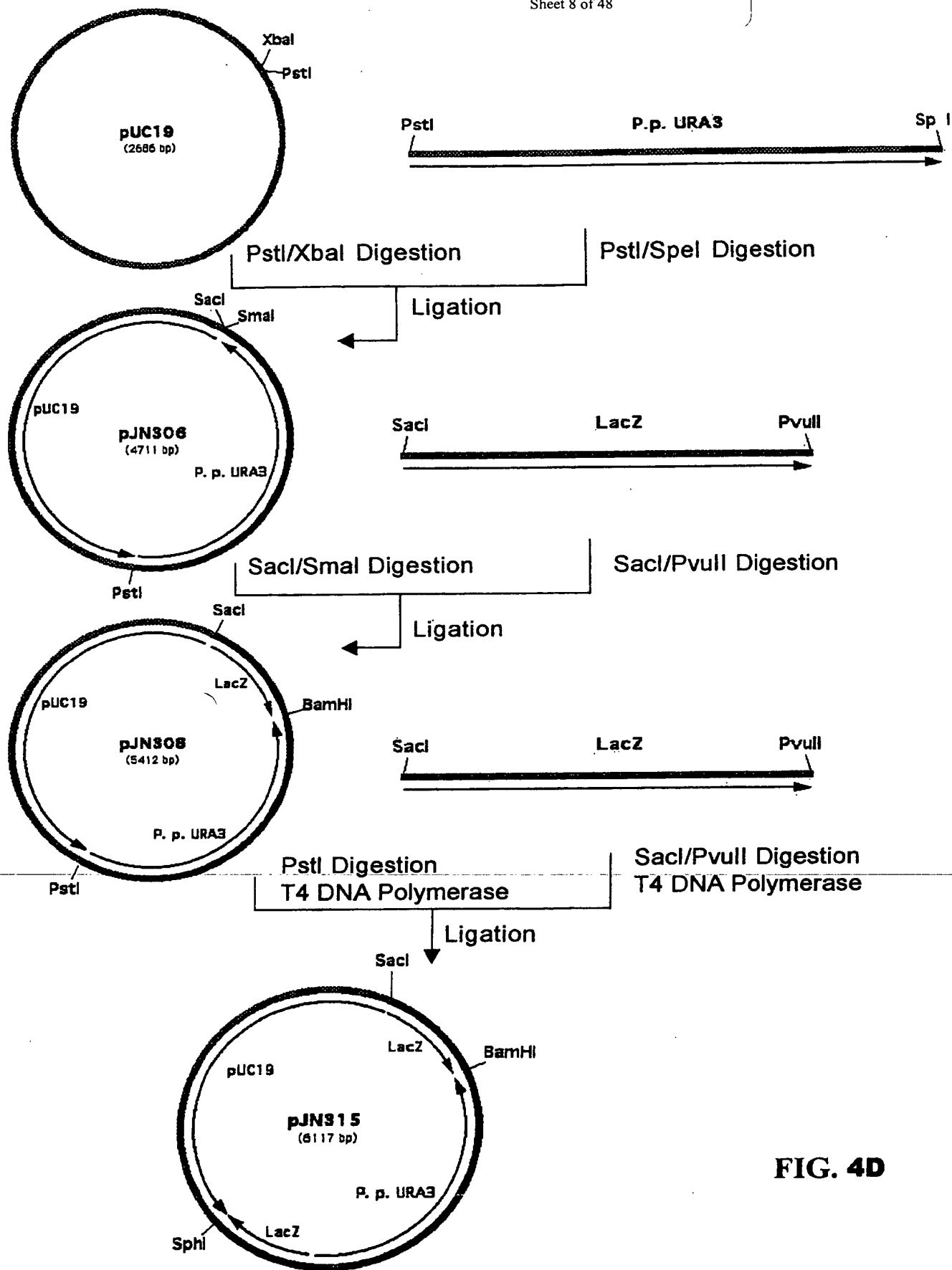


FIG. 4D

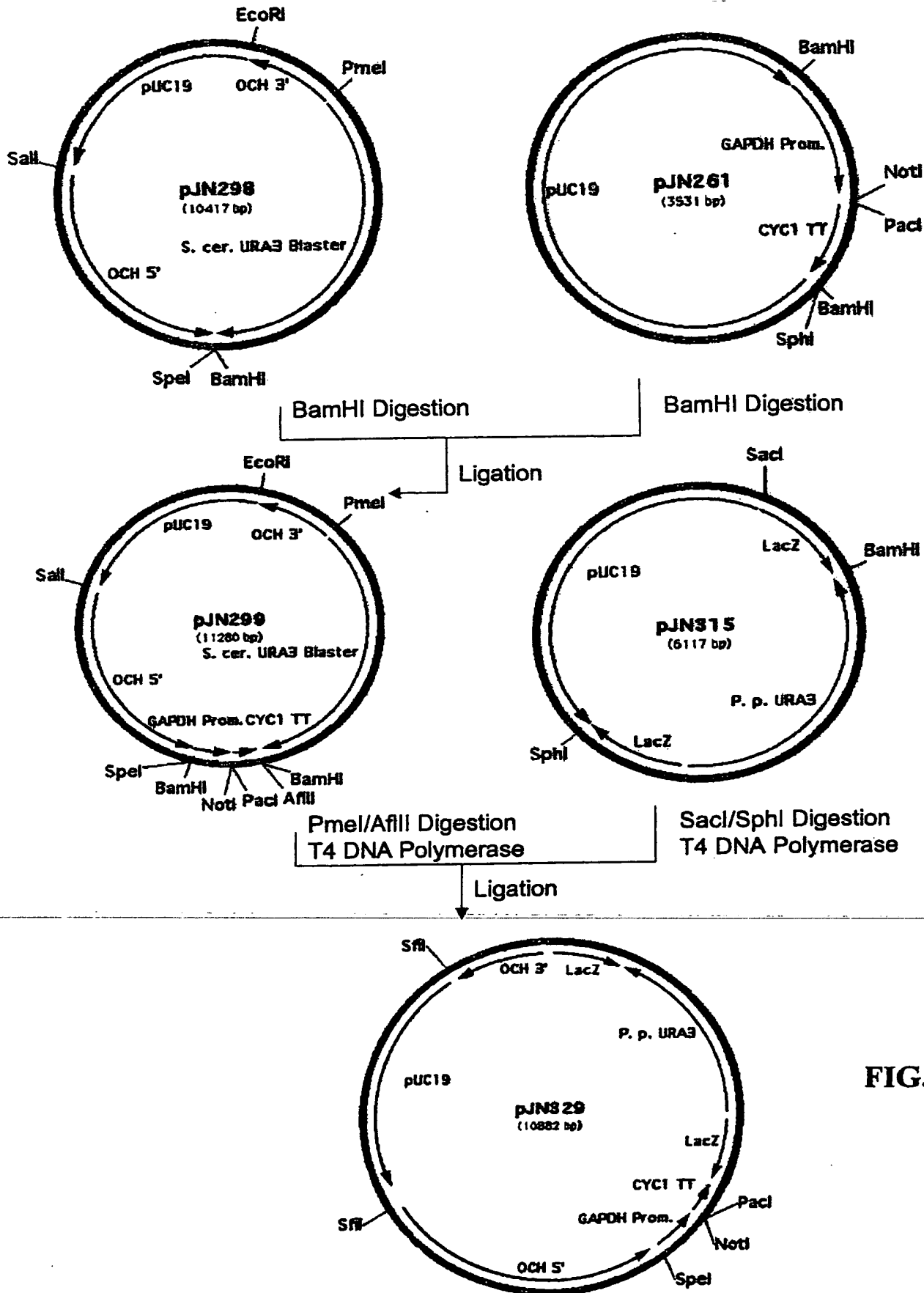


FIG. 4E

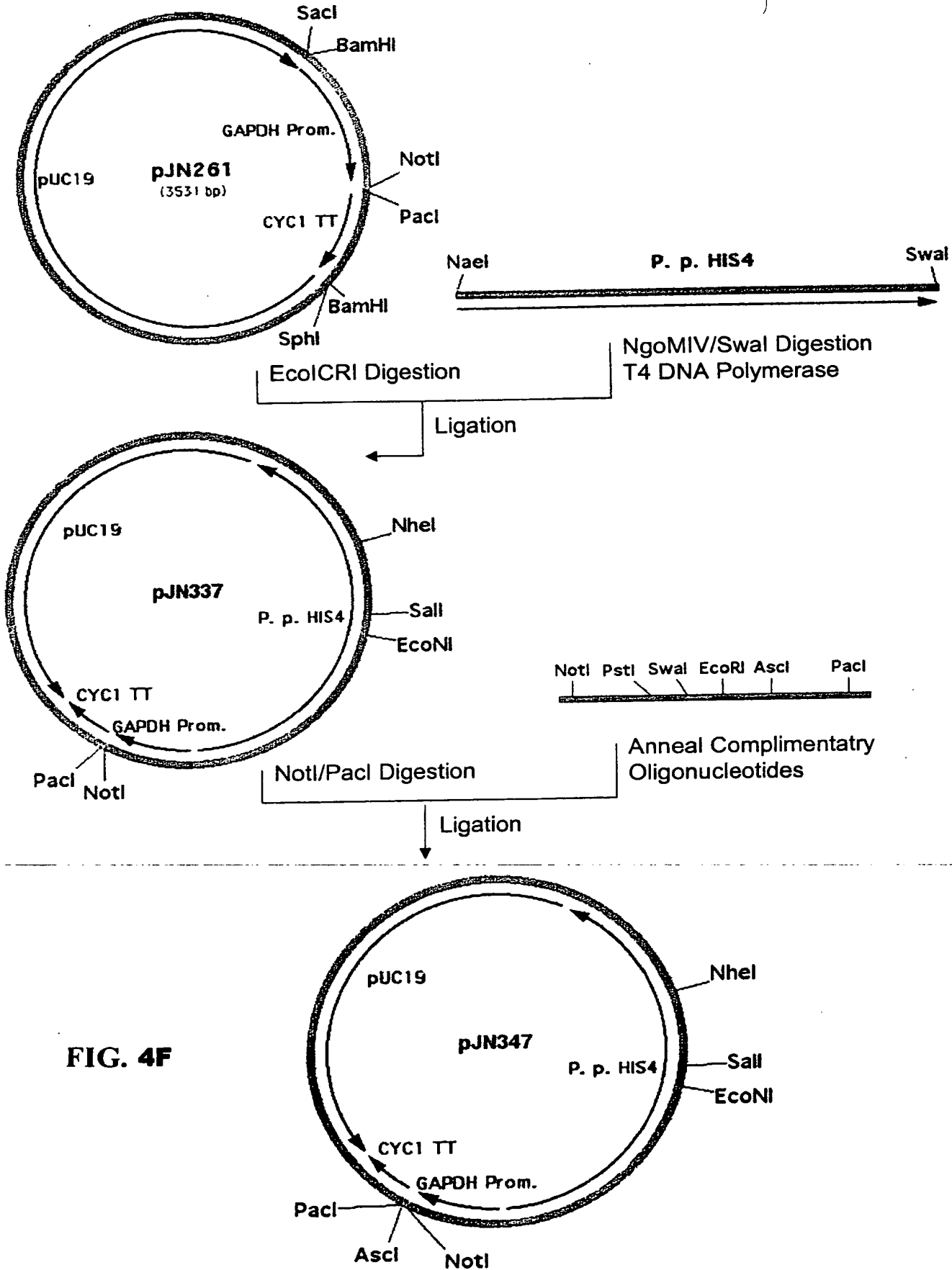


FIG. 4F

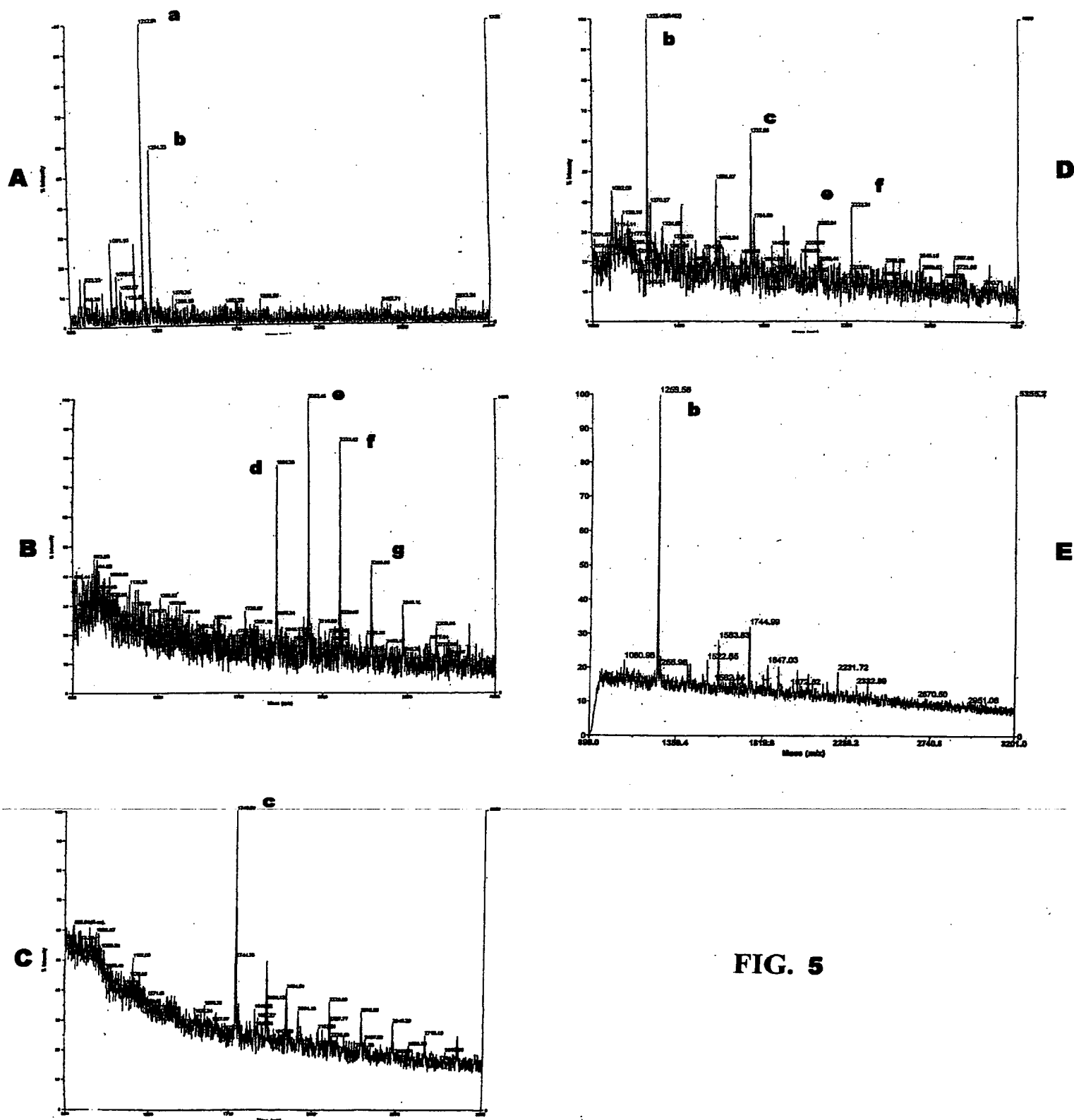
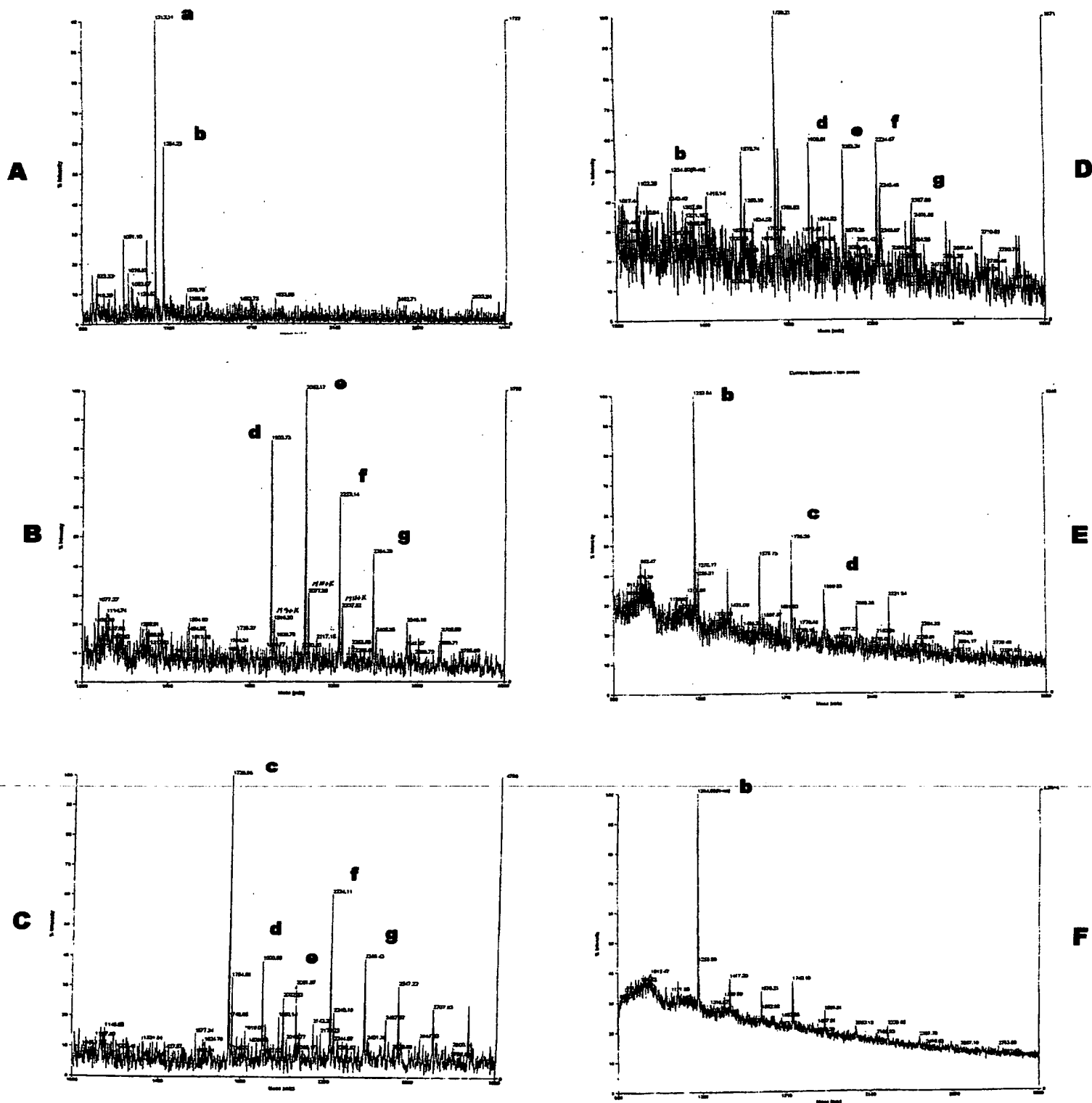
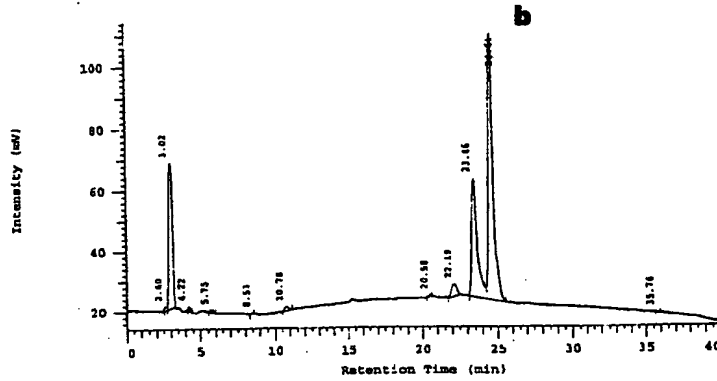


FIG. 5

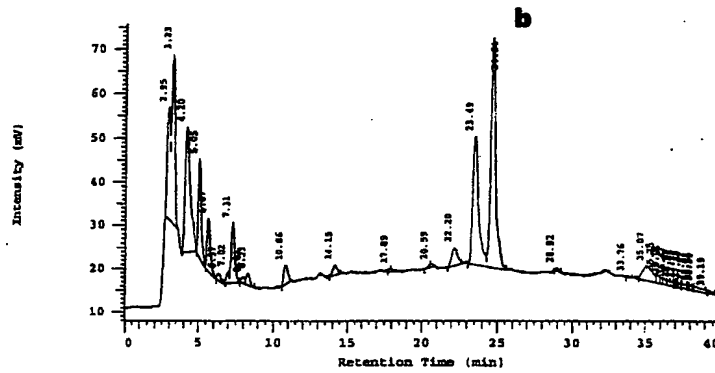
FIG. 6



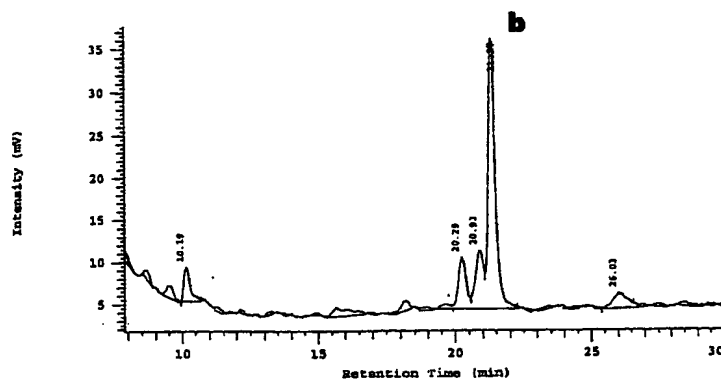
A



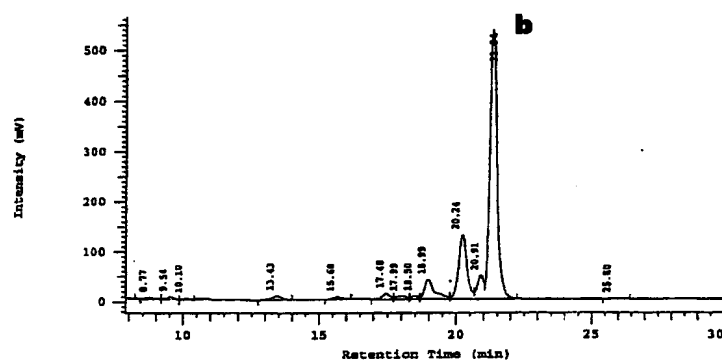
B



A



B



C

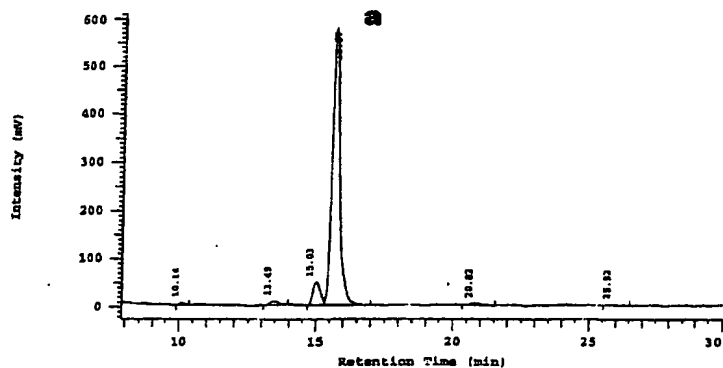
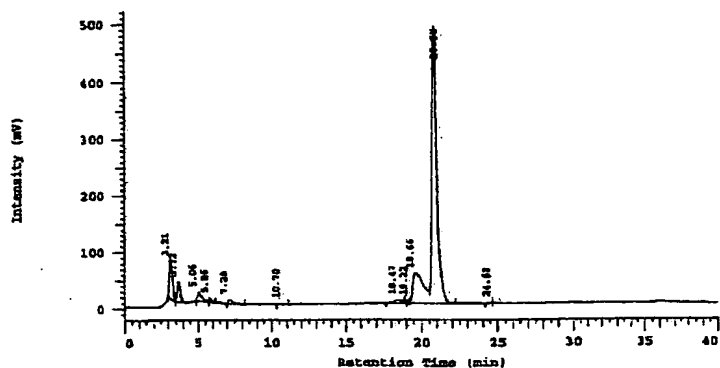
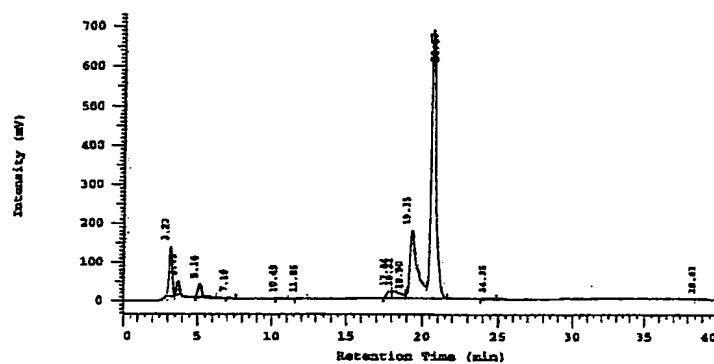


FIG. 8

A



B



C

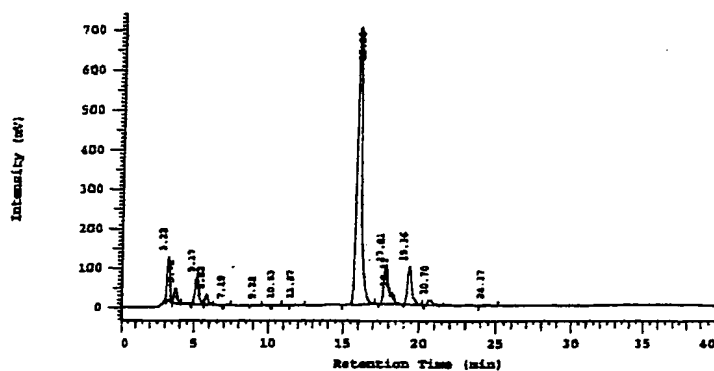
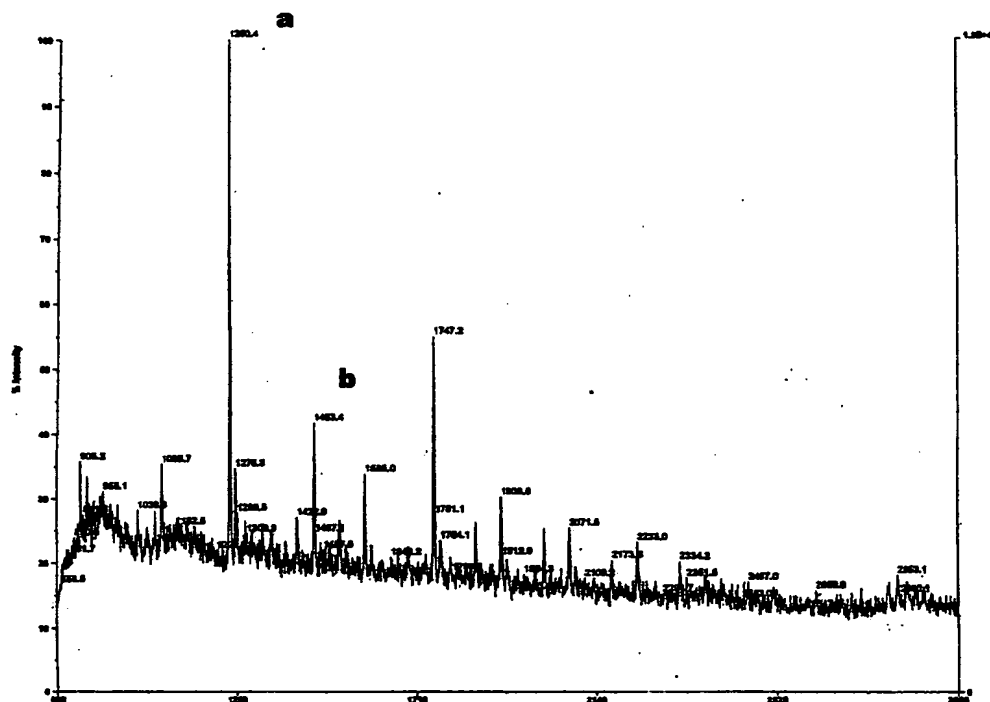
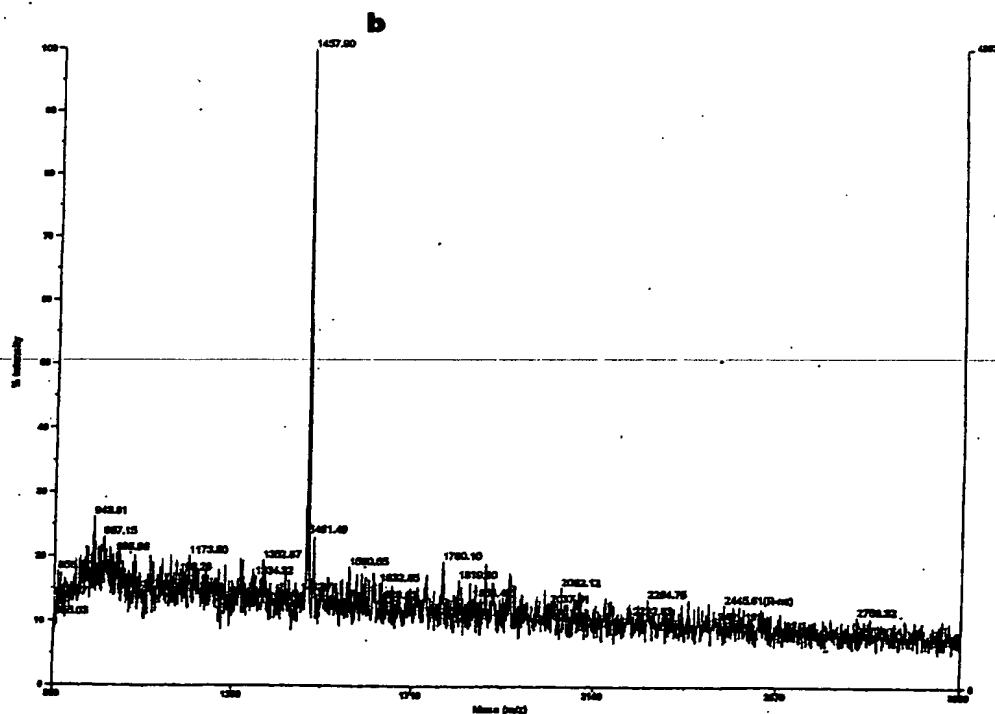


FIG. 9

FIG. 10



A



B

pH optimum for BB27-2 medium
C. elegans Mann1B D31 and S. Mnn10-s

pH	% f Man5
4.5	0
5	32
5.5	41
6	35
6.43	22
6.5	4
7.5	0
8.5	0

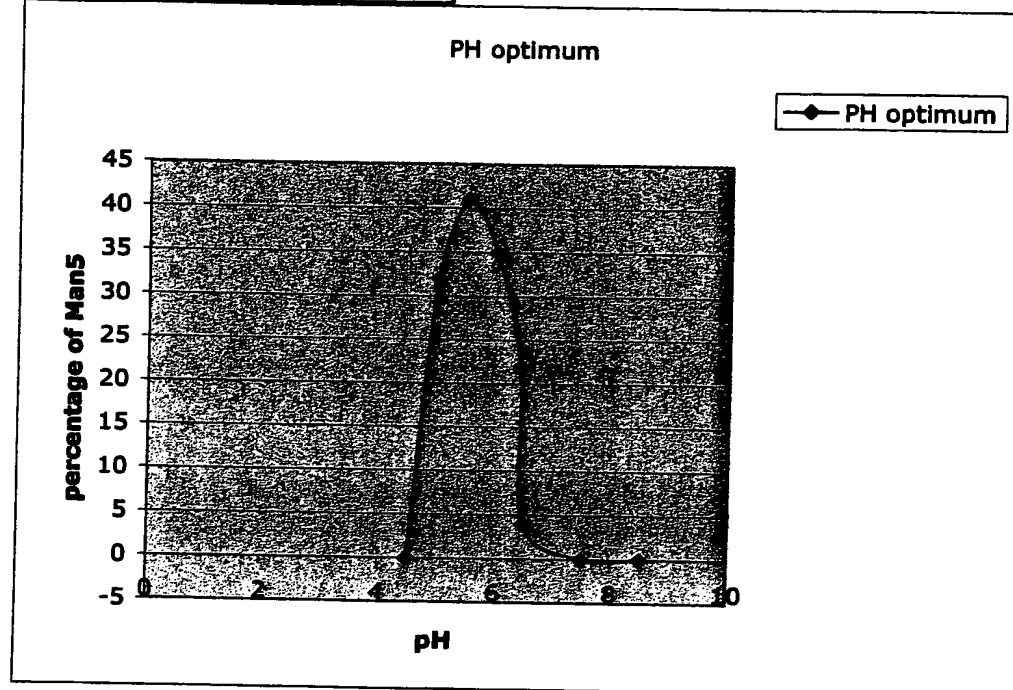
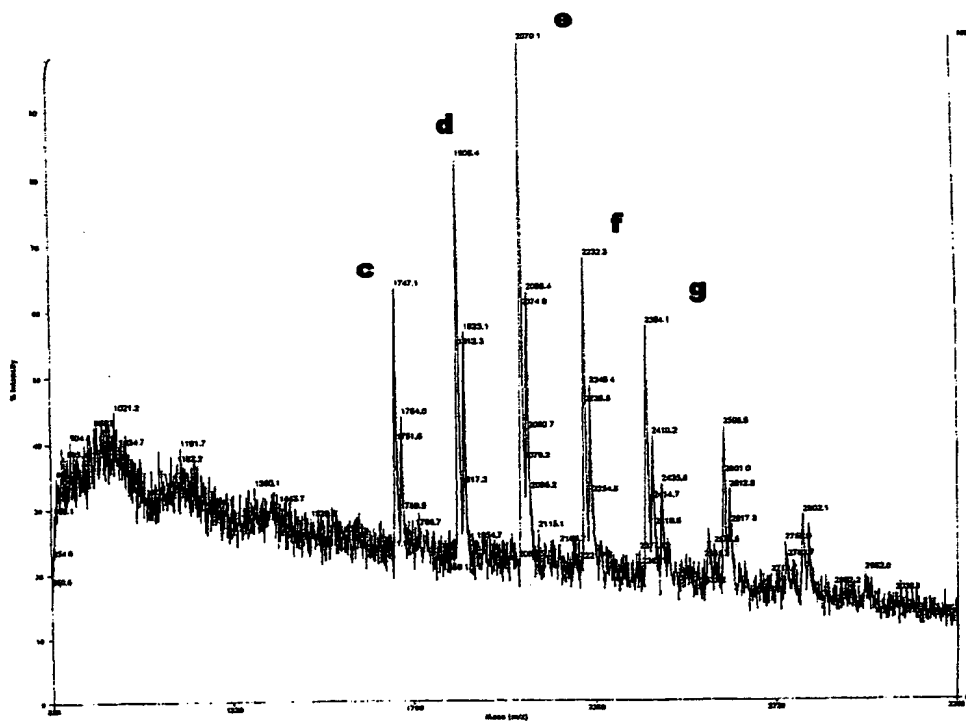
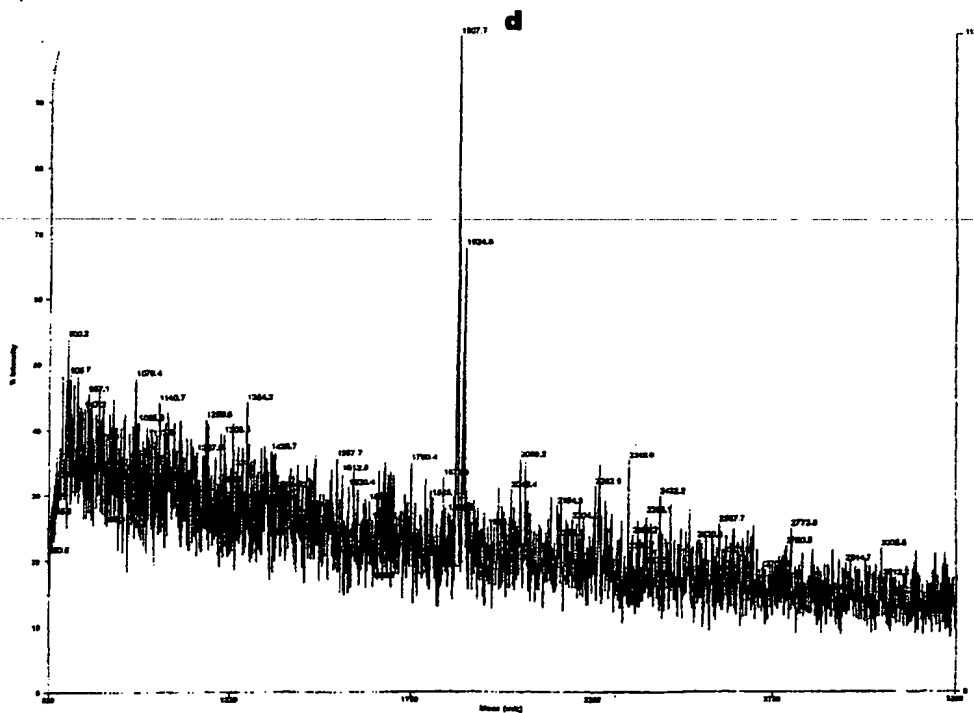


FIG. 11



A

FIG. 12



B

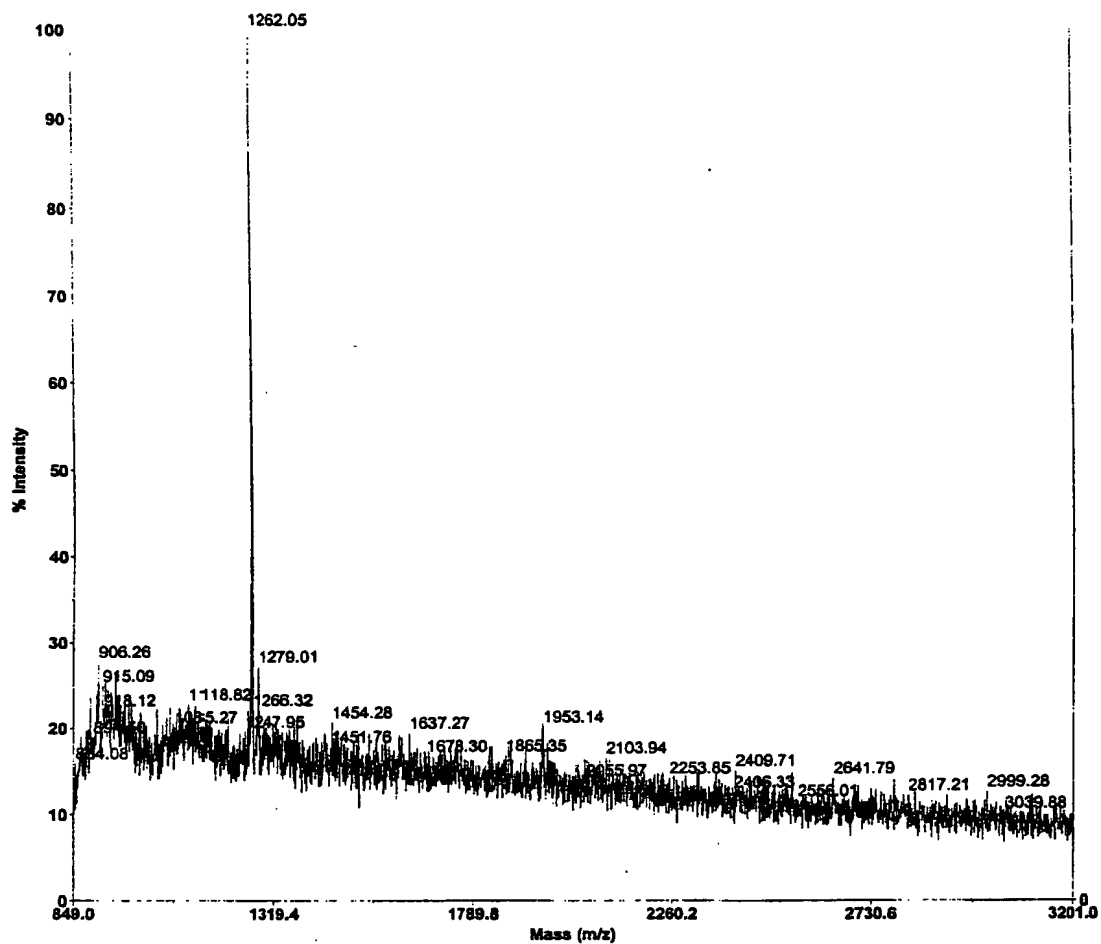


FIG. 12C

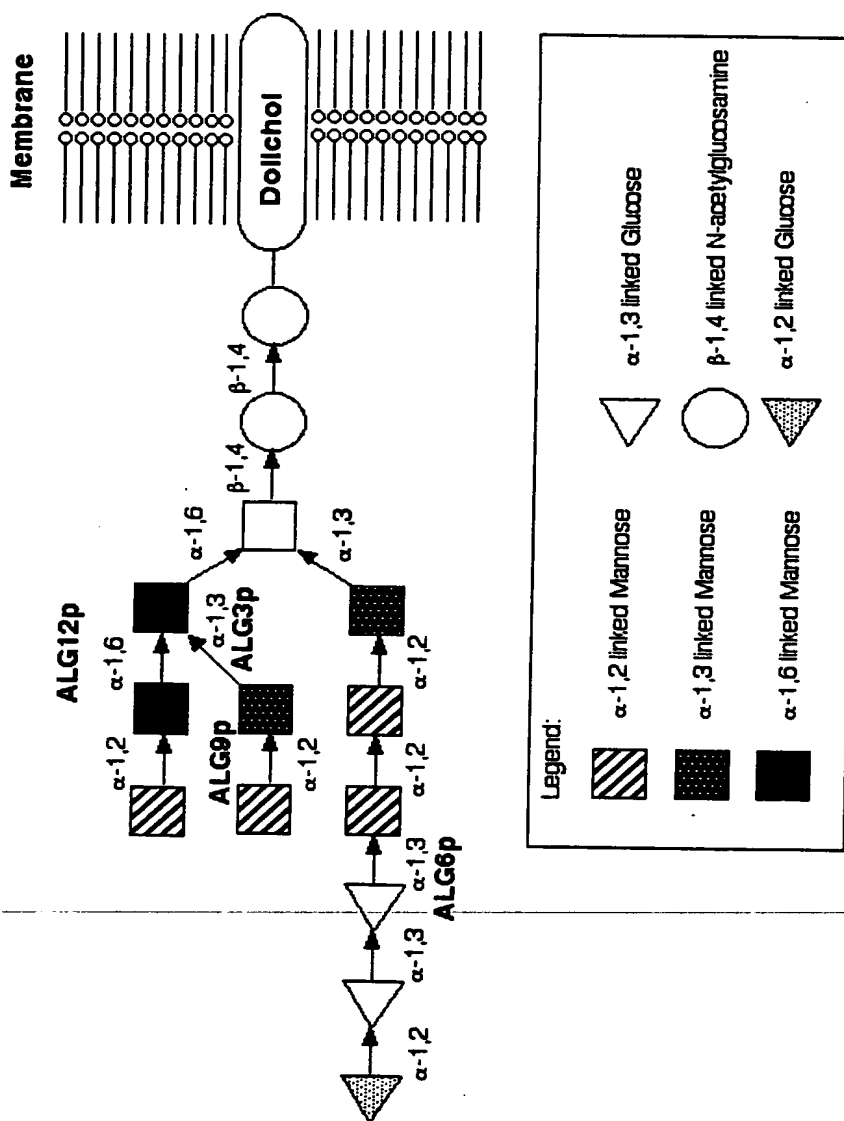


FIG. 13

Lipid-linked N-glycans

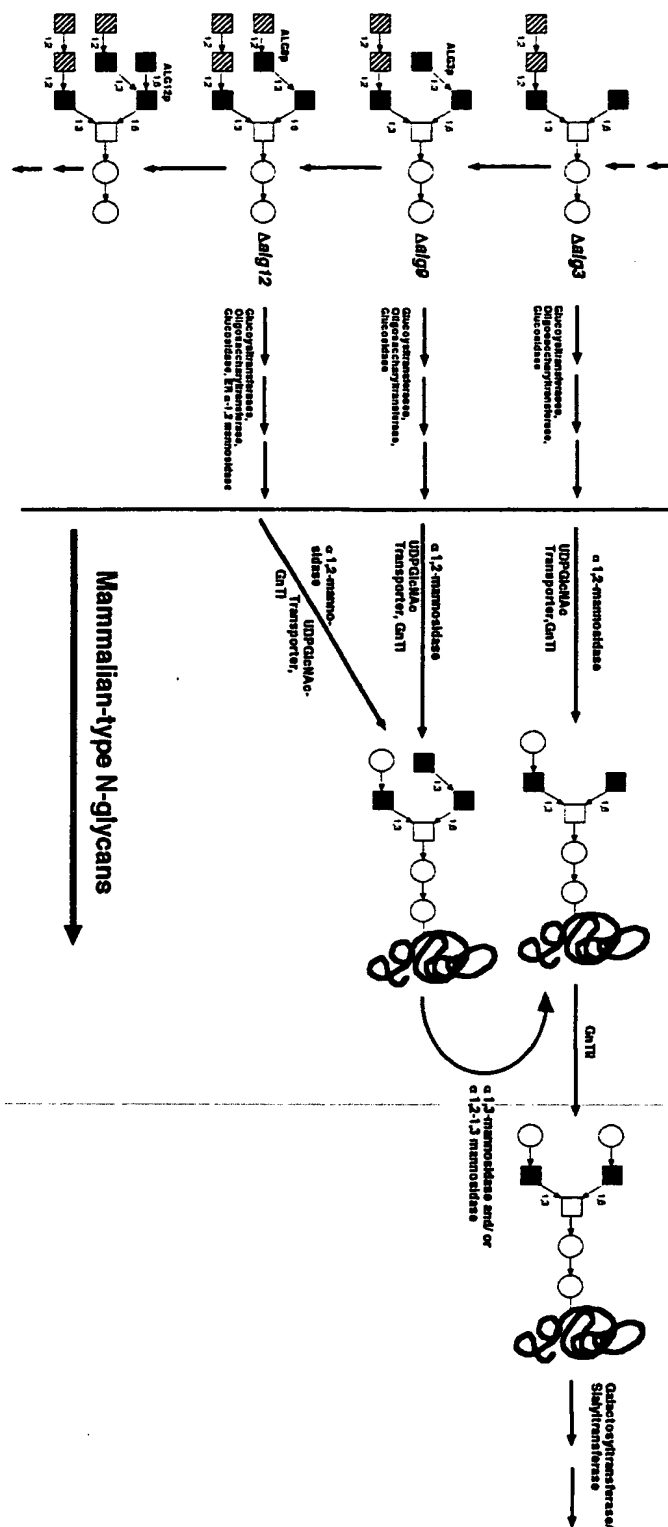


FIG. 14

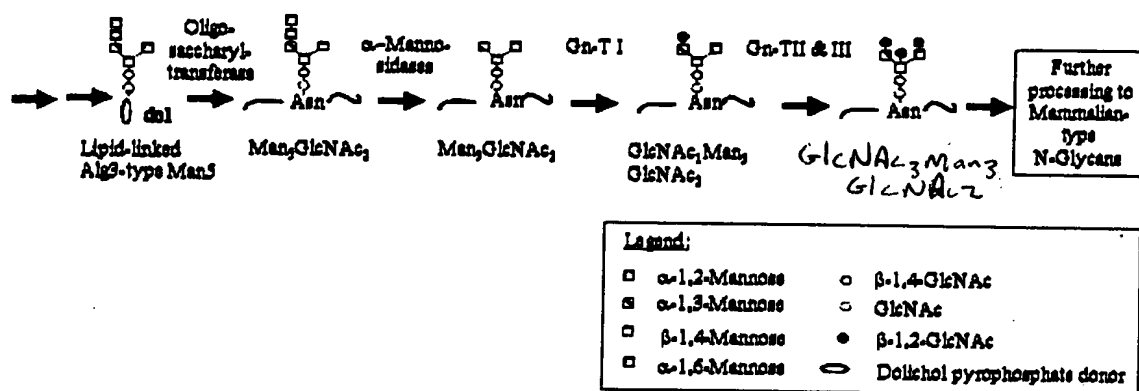


FIG. 15

ALG3 Blast 05-22-01

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3_YEAST	DOLICHYL-P-MAN:MAN(5)GLCNAC(...797	0.0
gi 3024226 sp Q92685 ALG3_HUMAN	DOLICHYL-P-MAN:MAN(5)GLCNAC...173	7e-43
gi 3024221 sp Q24332 NT56_DROVI	LETHAL(2)NEIGHBOUR OF TID P...145	3e-34
gi 3024222 sp Q27333 NT56_DROME	LETHAL(2)NEIGHBOUR OF TID P...121	3e-27
gi 10720153 sp P82149 NT53_DROME	LETHAL(2)NEIGHBOUR OF TID ...121	5e-27
gi 1707982 sp P40989 GLS2_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 32	2.8
gi 1346146 sp P38631 GLS1_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 31	6.6

Alignments

Yeast

>gi|586444|sp|P38179|ALG3_YEAST DOLICHYL-P-
 MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE
 (DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
 (HM-1 KILLER TOXIN RESISTANCE PROTEIN)
 Length = 458

Score = 797 bits (2059), Expect = 0.0
 Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLLILFESMLCKI	60
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLLILFESMLCKI	60
Query: 61	I I K K V A Y T E I D Y K A Y M E Q I E M I Q L D G M L D Y S Q V S G G T G P L V P A G H V L I Y K M M Y W L T E G M	120
Sbjct: 61	I I K K V A Y T E I D Y K A Y M E Q I E M I Q L D G M L D Y S Q V S G G T G P L V P A G H V L I Y K M M Y W L T E G M	120
Query: 121	D H V E R G Q V F F R Y L Y L L T L A L Q M A C Y Y L L H L P P W C V V L A C L S K R L H S I Y V L R L F N D C F T T L	180
Sbjct: 121	D H V E R G Q V F F R Y L Y L L T L A L Q M A C Y Y L L H L P P W C V V L A C L S K R L H S I Y V L R L F N D C F T T L	180
Query: 181	F M V V T V L G A I V A S R C H Q R P K L K K S L A L V I S A T Y S M A V S I K M N A L L Y F P A M M I S L F I L N D A	240
Sbjct: 181	F M V V T V L G A I V A S R C H Q R P K L K K S L A L V I S A T Y S M A V S I K M N A L L Y F P A M M I S L F I L N D A	240
Query: 241	N V I L T L L D L V A M I A W Q V A V A V P F L R S F P Q Q Y L H C A F N F G R K F M Y Q W S I N W Q M M D E E A F N D	300
Sbjct: 241	N V I L T L L D L V A M I A W Q V A V A V P F L R S F P Q Q Y L H C A F N F G R K F M Y Q W S I N W Q M M D E E A F N D	300
Query: 301	K R F X X X X X X X X X X X X X X F V T R Y P R I L P D L W S S L C H P L R K N A V L N A N P A K T I P F V L I A S N	360
Sbjct: 301	K R F H L A L L I S H L I A L T T L F V T R Y P R I L P D L W S S L C H P L R K N A V L N A N P A K T I P F V L I A S N	360
Query: 361	F I G V L F S R S L H Y Q F L S W Y H W T L P I L I F W S G M P F F V G P I W Y V L H E W C W N S Y P P N S Q X X X X X	420
Sbjct: 361	F I G V L F S R S L H Y Q F L S W Y H W T L P I L I F W S G M P F F V G P I W Y V L H E W C W N S Y P P N S Q	420
Query: 421	X X X X X X X X X X X X X X S G S V A L A K S H L R T T S S M E K K L N	458
Sbjct: 421	L A L N T V L L L L L A L T Q L S G S V A L A K S H L R T T S S M E K K L N	458

Human

>gi|3024226|sp|Q92685|ALG3_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL
 MANNOSYLTRANSFERASE

(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)

(NOT56-LIKE PROTEIN)

Length = 438

Score = 173 bits (439), Expect = 7e-43

Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85
 WQ+ R ++ + R L+V L L E + +I +VAYTEID+KAYM ++E + ++
 Sbjct: 29 WQER----RLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACY 145
 G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L Y
 Sbjct: 84 GTYDYTQLQGDGTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNI FAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPPWC-VVLACL SKRLHSIYVLRFLNDCFTTFLMVVTVLGAIVASRCHQRPKLKK 203
 + +PP+ + C S R+HSI+VLRFLND + + +L + QR
 Sbjct: 144 HQTKVPPFVFFFMCCASYRVHSIFVLRFLNDP-----VAMVLLFLSINLLLAQRWGWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPF 263
 +S+AVS+KMN LL+ P ++ L L L + A + QV + +PF
 Sbjct: 198 -----CCFFSLAVSVKMNVLFLFAPGLLFLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQQYLHCAFNFGRKFMYQWSINWQMDDEAFNDKRFXXXXXXXXXXXXXXXXXVTRY 323
 L P YL +F+ GR+F++ W++NW+ + E F + F + R+
 Sbjct: 250 LLENPSGYLSRSFDLGRQFLFHWTVNWRFLPEALFLHRAFLALLTAHLTLLLLFALCRW 309

Query: 324 PRILPDWSSLCHPLRKNVLANPAKTIPFVLIASNFIGVLFSSRLHYQFLSWYHWTLP 383
 R + S L P ++ I L SNFIG+ FSSRLHYQF WY TLP
 Sbjct: 310 HRTGESILSLLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSSRLHYQFYVWYFHTLP 369

Query: 384 ILIF-----WSGMPFFVGPVIWYVLHEWCWNSYPPNS 414
 L++ W + + + E WN+YP S
 Sbjct: 370 YLLWAMPARWLTHLLRLVLGLI--ELSWNTYPSTS 403

Drosophila Vi

>gi|3024221|sp|Q24332|NT56_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)
 Length = 526

Score = 145 bits (366), Expect = 3e-34

Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92
 ++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS
 Sbjct: 34 IKYLAPEPAALPIVSVLIVLAEAVINVLIQRPVTEIDWKAYMQECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LP 151
 + G TGPLVYPA V IY +Y+LT +V Q F +YLL + L + Y +P
 Sbjct: 93 LRGDTGPLVYPAAFVYIYSGLYYLTGQGTNVRQAQYIFACIYLLQMCVLRLYTKSRKVP 152

Query: 152 PWCVVLAACL-SKRLHSIYVLRFLNDCFTTFLMVVTVLGAIVASRCHQRPKLKSLALVIS 210
 P+ +VL+ S R+HSIYVLRFLND L +L A + QR L S
 Sbjct: 153 PYVLVLSAFTSYRIHSIYVLRFLNDPVAIL-----LLYAALNLFQDQRTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQ 270
 YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +
 Sbjct: 201 ICYSLAVGVKMN--ILLFAPALLLFYLANLGLVRLTLVQLTICAVLQLFIGAPFLRTHPME 258

Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 YL +F+ GR F ++W++N++ + +E F + F
 Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06
 Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPIILIFWSGMPFFVGPIWYVLH--EWCWNS 409
 +PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+
 Sbjct: 412 LPFFL--CNFIGVACARSRLHYQFYIWFHSLPYLV-WS-TPYSLGVRYLILGLIEYCWNT 467

Query: 410 YP 411
 YP
 Sbjct: 468 YP 469

Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)
 (NOT45)

Length = 510

Score = 121 bits (305), Expect = 3e-27
 Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPLLLIFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQV 93
 +Y++ + A IV ++L E ++ ++I++V YTEID+ AYM++ E L+G +YS +
 Sbjct: 36 KYLLLEPAALPIVGLFVLLAELVINVVVIRVPYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LPP 152
 G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP
 Sbjct: 95 RGD TGPLVYPAAFVYIYSALYYVTSHGTNVRLAQYIFAGIYLLQLALVLRLYSKSRKVPP 154

Query: 153 WCVLVACL-SKRLHSIYVLRFLFNDCTTFLFMVVTVLGAIVASRCHQRPKLKKSLLALVISA 211
 + +VL+ S R+HSIYVLRFLFND + V +L A + +R L S
 Sbjct: 155 YVLVLSAFTSYRIHSIYVLRFLFNDP-----VAVLLLYAALNLFDRRTLG-----ST 202

Query: 212 TYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQY 271
 +S+AV +KMN + A + LF L + ++ T+L L Q+ + PFL + P +Y
 Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLLRTILQLAVCGVIQLLLGAFFLLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 L +F+ GR F ++W++N++ + + F ++ F
 Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05
 Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPIILIFWSGMPFFVGPIWYVLHEWCWNSYP 411
 +PF L N +GV SRSRLHYQF WY +LP L + + V + L E+CWN+YP
 Sbjct: 407 LPFFL--CNLVGVACSRSLHYQFYVWFHSLPYLAWSTPYSLGVRCLILGLIEYCWNTYP 464

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 28883317
Number of Sequences: 96469
Number of extensions: 1107545
Number of successful extensions: 2870
Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 5
Number of HSP's successfully gapped in prelim test: 11
Number of HSP's that attempted gapping in prelim test: 2839
Number of HSP's gapped (non-prelim): 23

length of query: 458
length of database: 35,174,128
effective HSP length: 45
effective length of query: 413
effective length of database: 30,833,023
effective search space: 12734038499
effective search space used: 12734038499
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 67 (30.4 bits)

FIG.16-4



S. cerevisiae ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTGAAAAGTCTCTGCAAAGGAAGC
AATTTGTCAGACCTCCGCTGGATCTGTGGCAGGATCTCAAGGACGGTGTG
CGCTACGTGATCTTCGATTGTAGGGCCAATCTTATCGTTATGCCCCTTTGTG
ATTTTGTTCGAAAGCATGCTGTGCAAGATTATCATTAAAGAGGTAGCTTAC
ACAGAGATCGATTACAAGGCGTACATGGAGCAGATCGAGATGATTCAGCT
CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAAACGGGGCCCGCTGG
TGTATCCAGCAGGCCACGTCTTGATCTACAAGATGATGTACTGGCTAACA
GAGGGAATGGACCACGTTGAGCGCGGGCAAGTGTTTTTCAGATACTTGTA
TCTCCTTACACTGGCGTTACAAATGGCGTGTTACTACCTTTTACATCTACC
ACCGTGGTGTGTGGTCTTGGCGTGCCTCTCTAAAAGATTGCACTCTATTTA
CGTGCTACGGTTATTCAATGATTGCTTCACTACTTTGTTTATGGTCGTCACG
GTTTTGGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTTAAA
GAAGTCCCTTGCGCTGGTGATCTCCGCAACATACAGTATGGCTGTGAGCA
TTAAGATGAATGCGCTGTTGTATTTCCCTGCAATGATGATTTCTCTATTTCAT
CCTTAATGACGCGAACGTAATCCTTACTTTGTTGGATCTCGTTGCGATGAT
TGCATGGCAAGTCGCAGTTGCAGTGCCCTTCCTGCGCAGCTTTCCGCAACA
GTACCTGCATTGCGCTTTTAATTTTCGGCAGGAAGTTTATGTACCAATGGAG
TATCAATTGGCAAATGATGGATGAAGAGGCTTTCAATGATAAGAGGTTCC
ACTTGCCCTTTTAATCAGCCACCTGATAGCGCTCACCACACTGTTTCGTCA
CAAGATACCCTCGCATCCTGCCCGATTTATGGTCTTCCCTGTGCCATCCGC
TGAGGAAAAATGCAGTGCTCAATGCCAATCCCGCCAAGACTATTCCATTC
GTTCTAATCGCATCCAACCTTCATCGGCGTCCTATTTTCAAGGTCCCTCCAC
TACCAGTTTCTATCCTGGTATCACTGGACTTTGCCTATACTGATCTTTTGGT
CGGGAATGCCCTTCTTCGTTGGTCCCATTGTTGACGTCTTGCACGAGTGGT
GCTGGAATTCCTATCCACCAAACCTCACAAGCAAGCACGCTATTGTTGGCA
TTGAATACTGTTCTGTTGCTTCTATTGGCCTTGACGCAGCTATCTGGTTCGG
TCGCCCTCGCCAAAAGCCATCTTCGTACCACCAGCTCTATGGAAAAAAAG
CTCAACTGA

S. cerevisiae Alg3p

MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLIL
FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGM LDYSQVSGGTGPLVYPAG
HVLIIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLHLPPWCV
VLACLSKRLHSIYVLRFLNDCFTTFLMVVTVLGAIVASRCHQRPKLKSLALV
ISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVA
VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRFHLALLISHL
IALTTFLVTRYPRILPDLWSSLCHPLRKNVNLNANPAKTIPFVLIASNFIGVLFS
RSLHYQFLSWYHWTLPIIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL
LLALNTVLLLLLALTQLSGSVALAKSHLRTTSSMEKKLN

FIG. 17

P. pastoris ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAAGCTTACGCTGAAAAATGT
TATCGGTGATCTAGTGGCTCTTATTCAAAACGTTTATTTAACCCAGATTTT
AGTGTCTTCGTTGCACCTCTTTTATGGTTAGCTGATTCCATTGTTATCAAGG
TGATCATTGGCACTGTTTCCTACACAGATATTGATTTTTCTTCATATATGCA
ACAAATCTTTAAAATTTCGACAAGGAGAATTAGATTATAGCAACATATTTG
GTGACACCGGTCCATTGGTTTACCCAGCCGGCCATGTTTCATGCTTACTCAG
TACTTTCGTGGTACAGTGATGGTGGAGAAGACGTCAGTTTCGTTCAACAA
GCATTTGGTTGGTTATACCTAGGTTGCTTGTTACTATCCATCAGCTCCTACT
TTTTCTCTGGCTTAGGGAAAATACCTCCGGTTTATTTTGTTTTGTTGGTAGC
GTCCAAGAGACTGCATTCAATATTTGTATTGAGACTCTTCAATGACTGTTT
AACAAACATTTTTGATGTTGGCAACTATAATCATCCTTCAACAAGCAAGTAG
CTGGAGGAAAGATGGCACAACCTATTCCATTATCTGTCCCTGATGCTGCAG
ATACGTACAGTTTAGCCATCTCTGTAAAGATGAATGCGCTGCTATACCTCC
CAGCATTCCTACTACTCATATATCTCATTGTGACGAAAATTTGATTAAAG
CCTTGGCACCTGTTCTAGTTTTGATATTGGTGCAAGTAGGAGTCGGTTATT
CGTTCATTTTACCGTTGCACTATGATGATCAGGCAAATGAAATTCGTTCTG
CCTACTTTAGACAGGCTTTTGAAGTTAGTCGCAATTTCTTTATAAGTGGA
CGGTTAATTGGCGCTTTTGGAGCCAAGAACTTTCAACAATGTCCATTTTC
ACCAGCTCCTGTTTGTCTCCATATTATTACGTTAGTCTTGTTTCATCCTCAA
GTTCTCTCTCCTAAAAACATTGGAAAACCGCTTGGTAGATTTGTGTTGGA
CATTTTCAAATTTTGGAGCCAACCTTATCTCCAACCAATATTATCAACGA
CCCAGAAAGAAGCCCAGATTTTGTTTACACCGTCATGGCTACTACCAACTT
AATAGGGGTGCTTTTTTGCAAGATCTTTACACTACCAGTTCCTAAGCTGGTA
TGCGTTCTCTTTGCCATATCTCCTTTACAAGGCTCGTCTGAAGTTTATAGCA
TCTATTATTGTTTATGCCGCTCACGAGTATTGCTGGTTGGTTTTCCAGCTA
CAGAACAAAGTTCCGCGTTGTTGGTATCTATCTTACTACTTATCCTGATTC
TCATTTTTACCAACGAACAGTTATTTCTTCTCAATCGGTCCCTGCAGAAA
AAAAGAATACATAA

P. pastoris Alg3p

MPPIEPAERP KLT LKNVIGDLV ALIQNVLFNPDFS VFVAPLLWLADSI VIKVIIG
TVSYTDIDESSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS
DGGEDVSFVQQAFGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIF
VLRLFNDCLTTF LMLATIILQQASSWRKDGTIPLSVPDAADTYS LAISVKMN
ALLYLPAFLLLIYLICDENLIKALAPVLVLILVQVGVGYSFILPLHYDDQANEIR
SAYFRQAFDFSRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKF
LSPKNIGKPLGRFVLDFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF
ARSLHYQFLSWYAFSLPYLLYKARLNFIAIIIVYAAHEYCWLVPATEQSSAL
LVSILLILILIFTNEQLFPSQSVP AEKKNT

FIG. 18

P. pastoris ALG3 BLAST

Sequences producing significant alignments: (bits) Value

qi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...	228	2e-58
qi 12802365 gb AAK07848.1 AF309689 10 putative NOT-56 manno...	212	8e-54
qi 984725 gb AAA75352.1 ORF 1	206	4e-52
qi 7492702 pir T39084 probable mannosyltransferase - fissi...	176	8e-43
qi 16226531 gb AAL16193.1 AF428424 1 At2g47760/F17A22.15 [A...	164	2e-39
qi 25367230 pir B84919 Not56-like protein [imported] - Ara...	164	3e-39
qi 25814791 emb CAB70171.2 Hypothetical protein K09E4.2 [C...	161	2e-38
qi 17535001 ref NP_496950.1 Putative plasma membrane membr...	160	3e-38
qi 1654000 emb CAA70220.1 Not56-like protein [Homo sapiens...	155	2e-36
qi 13279206 gb AAH04313.1 AAH04313 Unknown (protein for IMA...	154	2e-36
qi 22122365 ref NP_666051.1 hypothetical protein MGC36684 ...	150	3e-35
qi 21292031 gb EAA04176.1 agCP3388 [Anopheles gambiae str...	120	4e-26
qi 1780792 emb CAA71167.1 lethal(2)neighbour of tid [Droso...	114	3e-24

Alignments

S. cerevisiae

Score = 228 bits (580), Expect = 2e-58
 Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNVLFNPDFSVFVAPLLWLADSIKVIIGTVSYTDIDFSSYM 68
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM
 Sbjct: 20 RPPLDLWQ---DLKDGVRVVFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYSDGGEDVSFVQQAFGWLYLG 127
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL
 Sbjct: 77 EQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPVYFVLLVASKRLHSIFVLRLFNDCLTTFMLLATI---IILQ 184
 L L ++ Y+ L +PP VL SKRLHSI+VLRLFNDC TT M+ T+ I+
 Sbjct: 137 TLALQMACYY--LLHLPPWCVVLA CLSKRLHSIYVLRLFNDCFTTLFMVTVLGAIVAS 193

Query: 185 QASSWRKDGTTIPLSVPAADTYSLAISVKMNXXXXXXXXXXXXXXXXXCDENLIKALAPXX 244
 + K ++ L + + TYS+A+S+KMN D N+I L
 Sbjct: 194 RCHQRPKLKKSALVI---SATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLV 250

Query: 245 XXXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDFSRQFLYKWTNVNWRFLSQETFNNV 304
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQOYLHCAFNFGRKFMYQWSINWQMMDEEAFNDK-301

Query: 305 HFHQQLFALHIITL-VLFILKFLSPKNIGKPLGRFVLDFKFWKPTLSPTNIIN-DPERS 362
 FH L H+I L LF+ ++ R + D++ L ++N +P ++
 Sbjct: 302 RFHLALLISHLIALTTLFVTRY-----PRILPDLWSSLCHPLRKNVLANPAKT 351

Query: 363 PDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW
 Sbjct: 352 IPF---VLIASNFIGVLFARSRLHYQFLSWYHTLPILIFWSGMPFFVGPVIWYVLHEWCWN 408

Query: 423 VFPATEQSS 431
 +P Q+S
 Sbjct: 409 SYPPNSQAS 417



Neurospora crassa

Score = 212 bits (540), Expect = 8e-54
Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIVIKVIIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYP 94
S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G TGPLVYP
Sbjct: 33 SKLIPPALFLVDALLCGLIIWKVPYTEIDWAAAYMEQVSQILSGERDYTEKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVA 154
A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL
Sbjct: 93 AAHVYIYTGLYHLTDEGRNILLAQQLFAGLYMVT LAVVMGCYW---QAKAPPYLFPLLT 149

Query: 155 SKRLHSIFVLRNFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPDAADTYSLAISVK 214
SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK
Sbjct: 150 SKRLHSIFVLRNFNDCAVLFVLAIFFFQR-RNWQA-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSFILPLHYDDQANEIRSAY 274
M + + L F+ HY + Y
Sbjct: 198 MTLTLLSLPAVGIVLFLGSG-SFVTTLQLVATMGLVQILIGVPFL--AHYPTE-----Y 247

Query: 275 FRQAFDFSQRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGK 333
+AF+ SRQF +KWTNVNWRF+ +E F + F L ALH++ L +FI +++ P K
Sbjct: 248 LSRAFELSRQFFFKWTNVNWRFVGEIIFLSKGFALTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLDIFKFWKPTLS-PTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWY 392
L + + + KP L+ P + + +P ++ T + + N +G+LFARSLHYQF ++
Sbjct: 306 SLVQLISPVLLAGKPPLTVPEHRAARDVTPRYIMTTILSANAVGLLFARSLHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIASIIIVYAAHEYCWLVPATEQSSA 432
A+S P+LL++A L+ + +++A HE+ W VFP+T SSA
Sbjct: 366 AWSTPFLLRAGLHPVLVYLLWAVHEWAWNVPSTPASSA 405

Schizosaccharomyces pombe

Score = 176 bits (445), Expect = 8e-43
Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIVIKVIIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101
L L + + II V YT+ID+ +YM+Q+ GE DY++ G TGPLVYP GHV Y
Sbjct: 30 LLLLEIPFVFAIISKVPYTEIDWIAAYMEQVNSFLLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161
++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI
Sbjct: 90 TLLYYLTDGGTNIVRAQYIFAFVYW--ITTAIVGYLFK-IVRAPFYIYVLLILSKRLHSI 146

Query: 162 FVLRNFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPDAADTYSLAISVKMNXXXXX 221
F+LRLFNDC + L + I+ W + A+ S+A SVKM+
Sbjct: 147 FILRLFNDCGNS-LFSSLFILSSCKKKWVR-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSFILPLHYDDQANEIRSAYFRQAFDF 281
L++ L P + + + +Y+ QAFDF
Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF----LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
R F YKWTNVNWRF+ + F + F + LH+ LV F K + + P
Sbjct: 243 GRAFDYKWTNVNWRFI PRSIFESTSFSTSILFLHVALLVAFCTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401
F L+ + +P+F++T +AT+NLIG+L ARSLHYQF +W+A+ PYL Y

Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWYSPYLCY 354

Query: 402 KARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
+A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384
Arabidopsis thaliana

Score = 164 bits (415), Expect = 2e-39
Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIVIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101
L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPYTKIDWDAYMSQVSGFLGGERDYGNLKGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDGGEDVSFVQQAFGWLYLGCLLLSISSYFFSGLGKIPVYFVLLVASKRLHSI 161
S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTGG--EVYPAQILFGVLYIVNLGIVLIIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPDAADTYSLAISVKMNXXXXX 221
FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMALFL----YRKWHLGMLV-----FSGAVSVKMNVLLEYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDF 281
N+I ++ F++ +Y AFD

Sbjct: 203 PTLLELLKAM--NIIGVVSALAGAALAIQILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLFLLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLL 400
F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSSLSFSDVSASRIITKEHVVTAMFVGNFIGIVFARSLHYQFYSWYFSLPYLL 370

Query: 401 YKARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRRLIMFLGIELCWNVPSTPSSS 401

FIG. 19-3



K. lactis ALG3

TTTGTTTACAAGCTGATACCAACGAACATGAATACACCGGCAGGTTTACT
GAAGATTGGCAAAGCTAACCTTTTACATCCTTTTACCGATGCTGTATTCAG
TGCGATGAGAGTAAACGCAGAACAAATTGCATACATTTTACTTGTTACCA
ATTACATTGGAGTACTATTTGCTCGATCATTACACTACCAATTCCTATCTT
GGTACCATTGGACGTTACCAGTACTATTGAATTGGGCCAATGTTCCGTATC
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAACACATACTG
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACCTCGAAAAGTGGTGATAA
CGAAACAACACACGAGAAAGCTGAG

K. lactis Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQIAYILLVTNYI
GVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLCVLWYLTHEWCWNSYPP
NATASTLLHACNTYCYWLYSZEDPQTRKVVITKQHTRKL

FIG. 20

K. lactis ALG3 BLAST

Score	E		(bits)	Value
Sequences producing significant alignments:				
gi 586444 sp P38179 ALG3_YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...)	125	1e-28	
gi 984725 gb AAA75352.1	ORF 1	94	4e-19	
gi 16226531 gb AAL16193.1 AF428424.1	At2g47760/F17A22.15 [A...	72	1e-12	
gi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72	1e-12	
gi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....	69	2e-11	
gi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65	2e-10	

Alignments

S. cerevisiae

Score = 125 bits (314), Expect = 1e-28
 Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)
 Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242
 ++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+
 Sbjct: 332 SSLCHPLRKNVAVLNANP--AKTIPFVLIASNFIGVLFARSRLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVPPYPLCVLWYLTHEWCWNSYPPNATASTLLHACNTYCYWLYS*EDPQTRKVVITKQHTR 422
 +P+ + +WY+ HEWCWNSYPPN+ ASTLL A NT L + + V + K H R
 Sbjct: 390 GMPFFVGPPIWYVLHEWCWNSYPPNSQASTLLALNTVLLLLLA-LTQLSGSVALAKSHLR 448

A. thaliana

Score = 72.0 bits (175), Expect = 1e-12
 Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)
 Frame = +3

Query: 84 FTDVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLC 263
 F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L
 Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGNFIGIVFARSLHYQFYSWYFYSLPYLLWRTPFPTWLR 380

Query: 264 VLWYLTHEWCWNSYPPNATASTL---LHACNTYCYWLYS*EDPQTRK 395
 ++ +L E CWN YP ++S L LH WL DP K
 Sbjct: 381 LIMFLGIELCWNVPSTPSSSGLLLCLHLIILVGLWLAPSVDPYQLK 427

FIG. 21

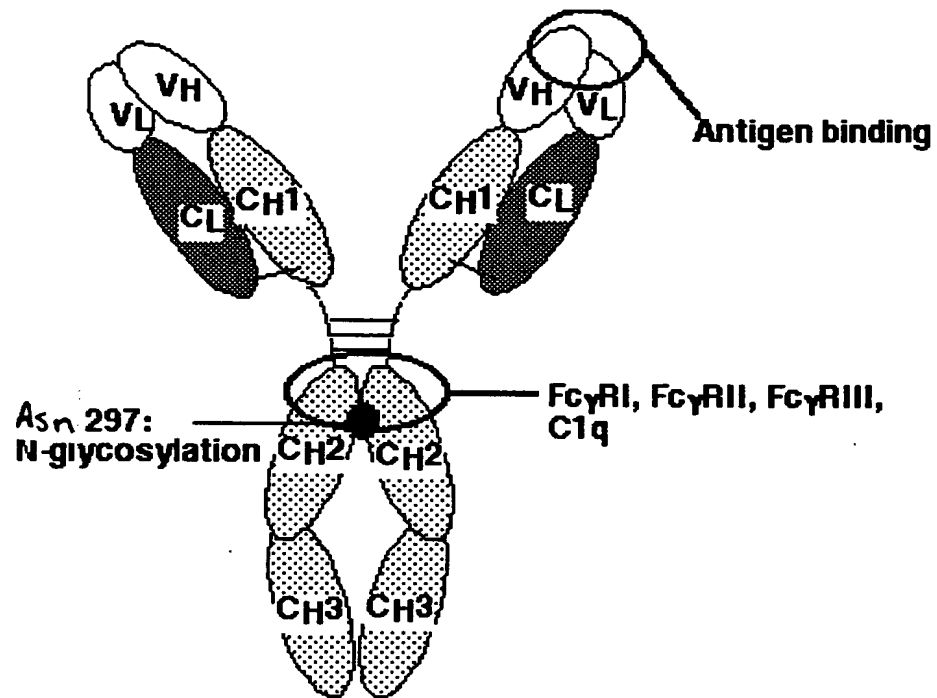


FIG. 22

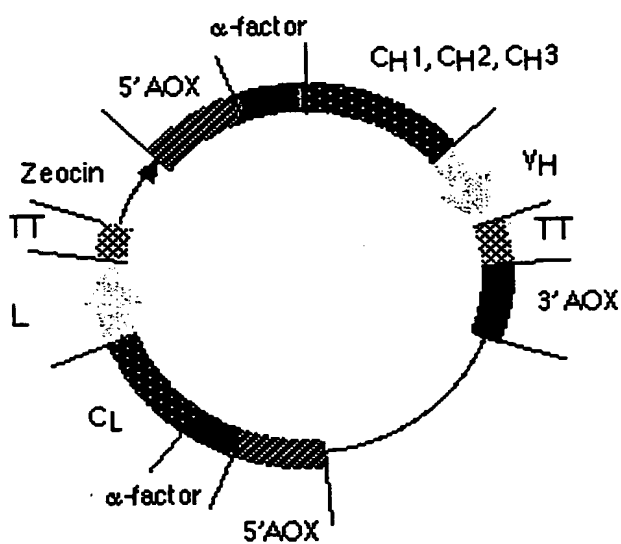


FIG. 23

>gi|6754685|ref|NM_010795.1| Mus musculus mannoside acetyl
glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTTCTCATGTTCTGTATGGCTGGCCTGTGCCTCATATCCTTCCTGC
ACTTCTTTAAGACCTTATCCTATGTACCTTCCCAGAGAACTGGCCTCCCTCAGCCCTAACCTCGTATC
CAGCTTCTTCTGGAACAATGCCCTGTCACTCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG
CGGACACCCCTCTACTCCCACTCTCCCTGCTCCAGCCACTGTCCCCGAGCAAGGCCACAGAGGAACTGC
ACCGGGTGGACTTCGTGTTGCCGGAGGACACCACGGAGTATTTTGTGCGCACCAAGCTGGTGGTGTGTG
CTTCAAACCAGGTACCAGGATGCTGGAGAAACCTTCGCCAGGGCGGACAGAGGAGAAGCCCGAAGTGTCT
GAGGGCTCCTCAGCCCGGGGACCTGCTCGGAGGCCATGAGGCACGTGTTGAGTACGCGGGAGCGCCTGG
GCAGCCGGGGCACTAGGCGCAAGTGGGTGAGTGTGTGTGCCTGCCAGGCTGGCACGGGCCAGTTGCGG
GGTGGCCACGGTGGTGCAGTATTCCAACCTGCCACCAAGGAACGCCTGGTACCCAGGGAGGTACCGAGG
CGGGTTATCAACGCCATCAACATCAACCACGAGTTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGGAG
ATGTTGTGGACGCCCTTCGTGGTCTGTGAATCTAATTTACCGCCTACGGGGAGCCTCGGCCGCTCAAGTT
CCGAGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTATGTCTTCTGGACCAT
TCCCACCTGGTGGCCGTCAGGACGGCTGGATTGCGGATGACTACCTGCGCACCTTCTCACCAGGATG
GCGTCTCCCGCCTGCGCAACCTGCGGCCCGATGACGTCTTTATCATCGACGATGCGGACGAGATCCCTGC
GCGTGATGGTGTGCTGTTCTCAAACTCTACGATGGCTGGACAGAGCCCTTCGCCTTCCACATGCGGAAG
TCCCTGTGGTCTTCTTCTGGAAGCAGCCGGGCACACTGGAGGTGGTGTGAGGCTGCACCATGGACATGC
TGCAGGCCGTGTATGGGCTGGATGGCATCCGCTGCGCCCGCCAGTACTACACCATGCCCAACTTCCG
GCAGTATGAGAACCGCACCGGCCACATCTAGTGAGTGGTCTCTCGGCAGCCCCCTGCACTTCGCGGGC
TGGCATTGCTCCTGGTGTCTTACACCCGAGGGCATCTACTTTAAACTCGTGTGAGCCAGAAATGGCGACT
TCCCCCGCTGGGGTGACTATGAGGACAAGAGGGACCTCAATTACATCCGCAGCTTGATCCGCAGTGGGG
ATGGTTTCGACGGAACGCAGCAGGAGTACCCTCCTGCGGACCCAGTGAGCACATGTATGCTCCTAAATAC
CTGCTCAAGAACTATGACCAGTTCCGCTACTTGCTGGAAAATCCCTACCGGGAGCCCCAAGAGCACTGTAG
AGGGTGGGCGCCAGAACCAGGGCTCAGATGGAAGGCCATCTGCTGTGAGGGGCAAGTTGGATACAGTGA
GGGCTAG

>gi|2117717|pir||JC4362 beta-1,4-mannosyl-glycoprotein 4-beta-N-
acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse
MRRYKFLMFCMAGLCLISFLHFFKTLSTVTFPRELASLSPNLISFFWNNAPVTPQASPEPGDPDLLRT
PLYSHSPLLQPLSPSKATEELHRVDFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSPGRTEEKTEVSEG
SSARGPARRPMRHLSSRERLGSRGTRRKWVECVCLPGWHGSPSCGVPTVVQYSNLPKTERLVPREVP
INAININHEFDLLDVRFHLDVDFVCDNFNTAYGEPRLKFRMLTNGTFEYIRHKVLYVFLDHF
PGGRQDGWIADDYLRFTLTQDGVSRRLNLRPDDVFIIDDADEIPARDGVLFLKLYDGTWTEPFAFHMRKSL
YGFQWKQPGTLEVVSGCTMDMLQAVYGLDGIRLRRRQYYTNPFRQYENRTGHILVQWSLGSPLHFA
GWHCSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRDNLNIRSLIRTGGWFDGTQOEYPPADPSEHMYAPKYL
KNYDQFRYLLENPYREPSTVEGGRQNGSDGRSSAVRGKLDTAEG

FIG. 24

Fig. 25

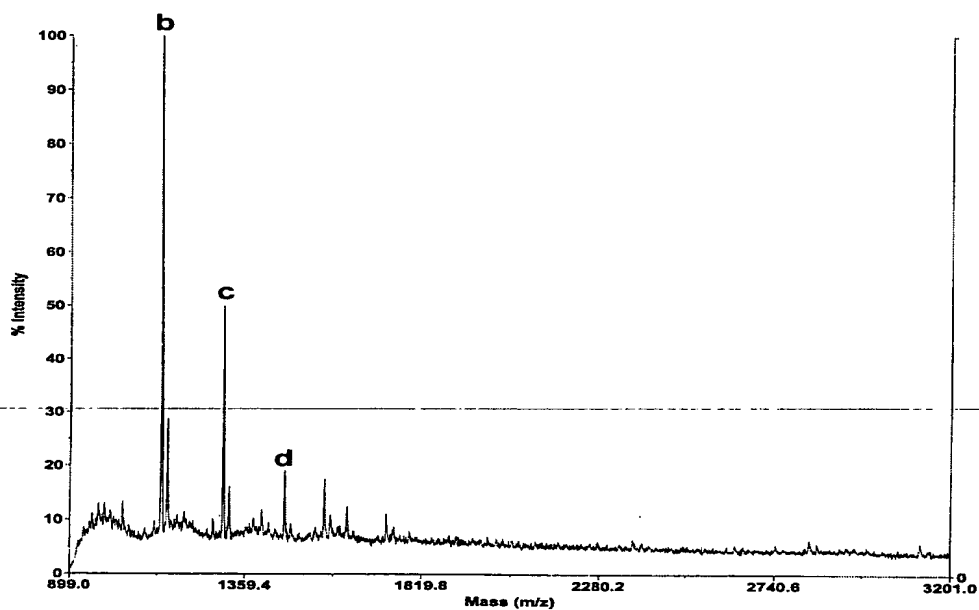
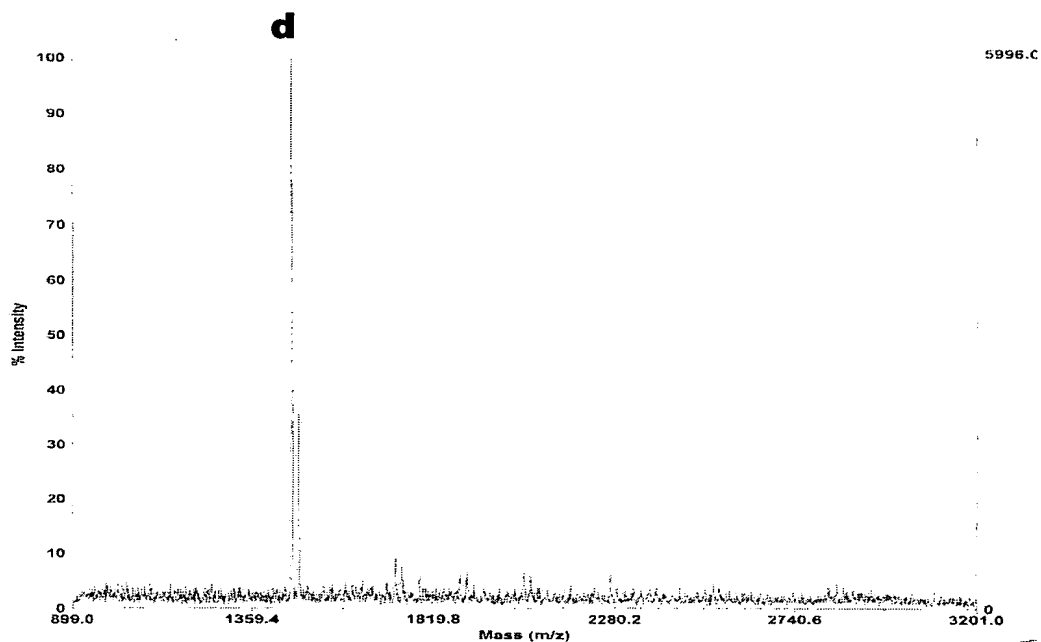


Fig. 26

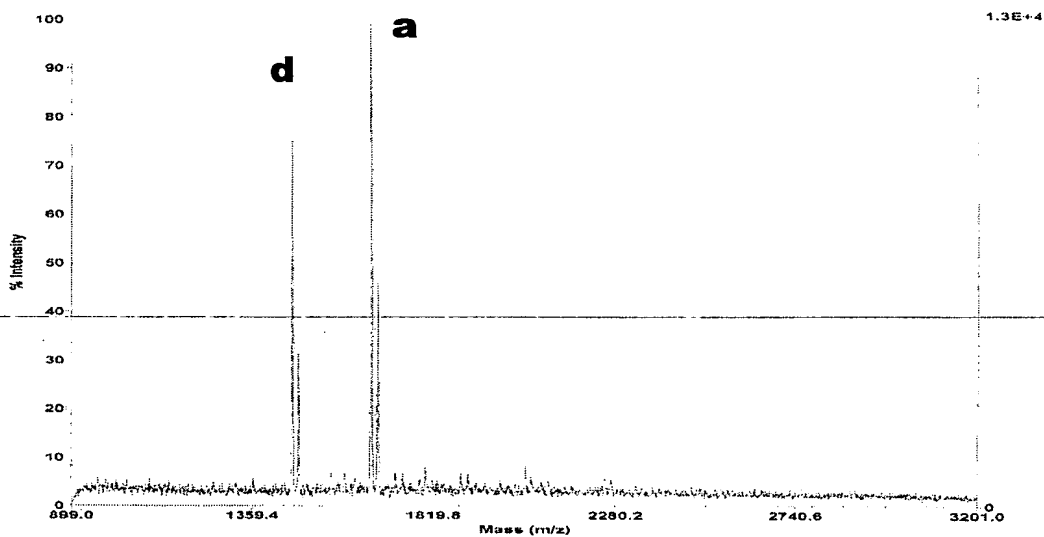
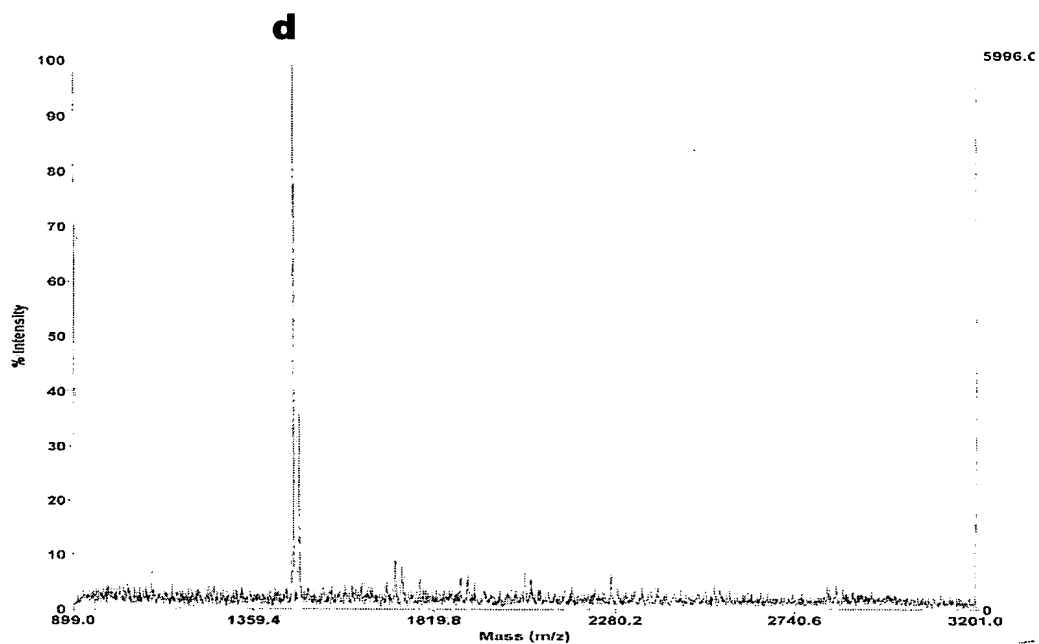


Fig. 27

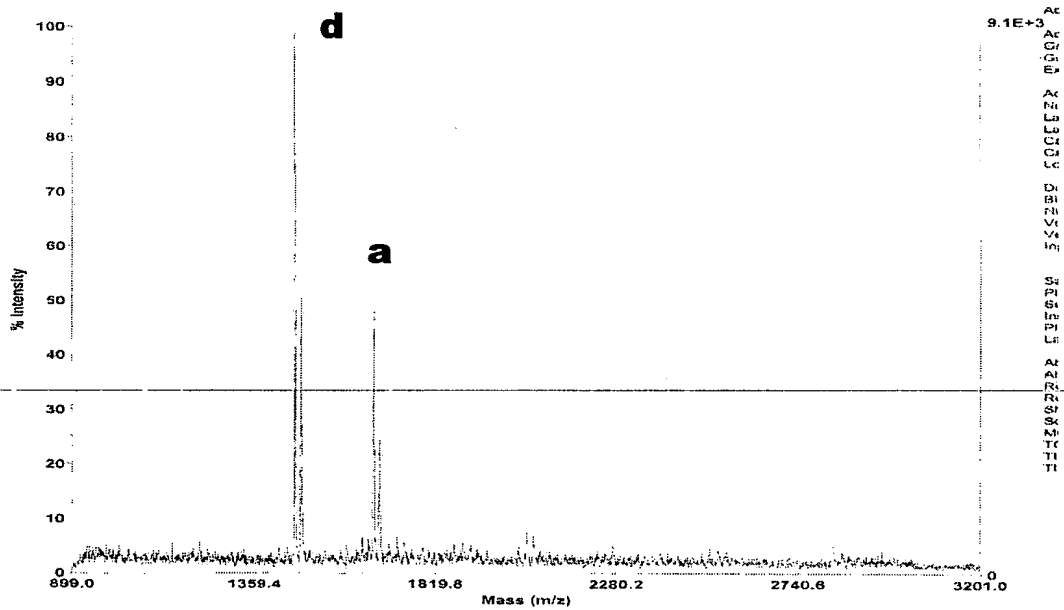
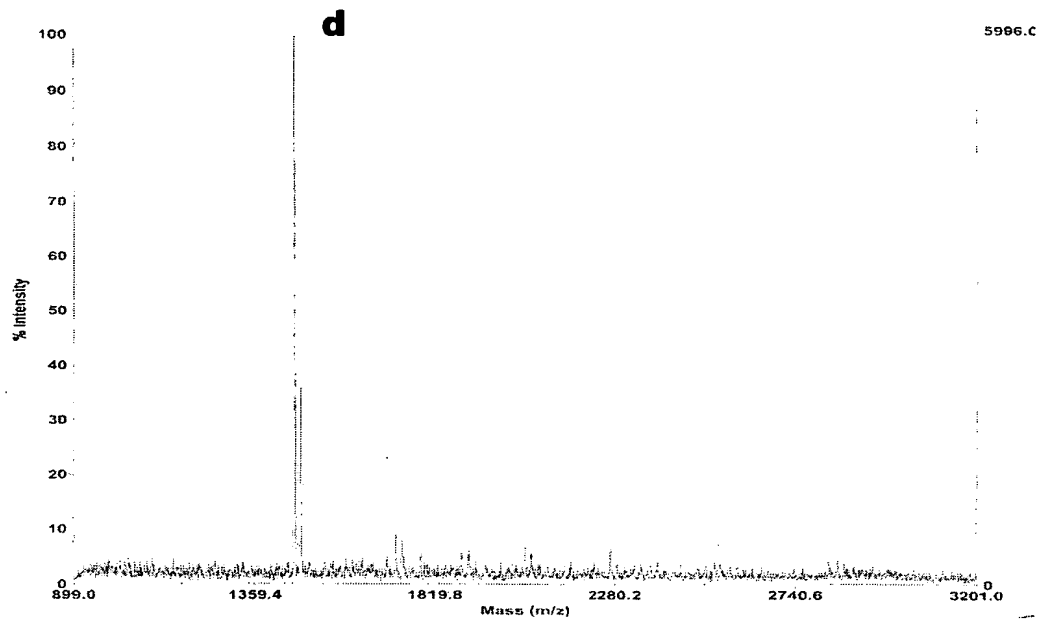


Fig. 28

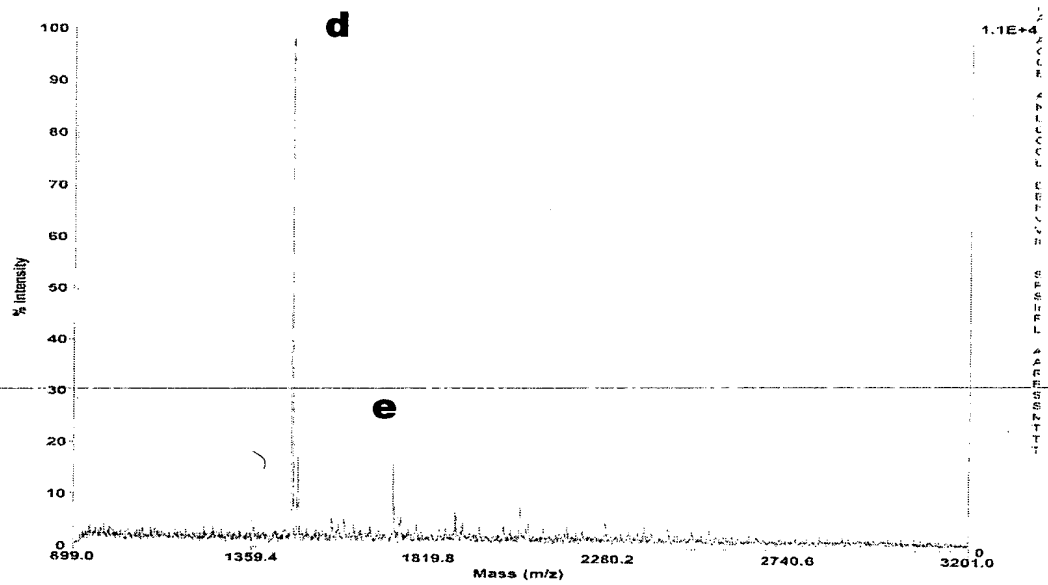
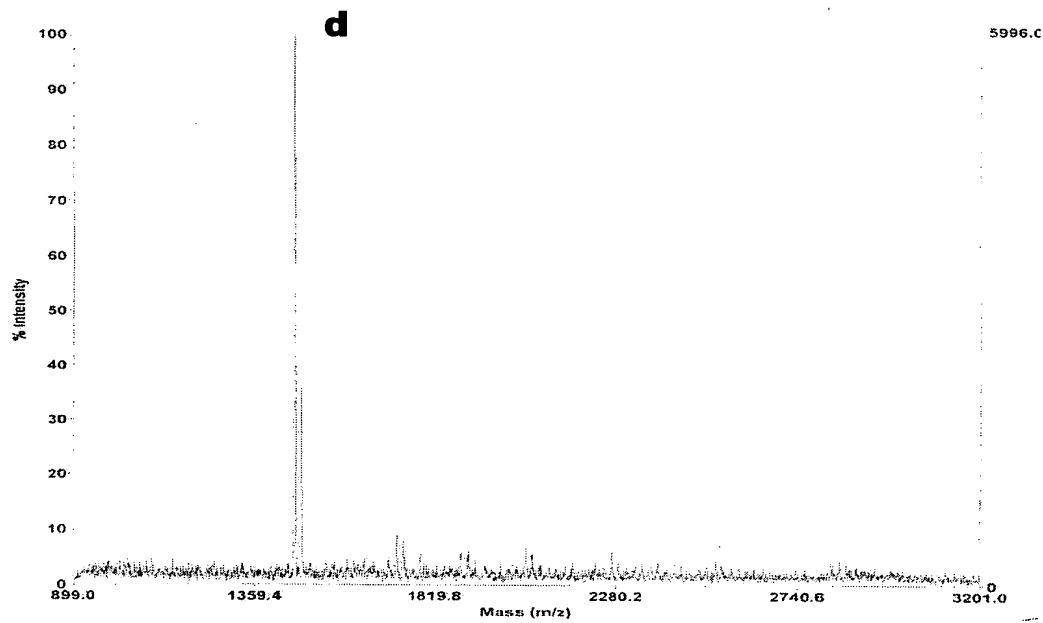


Fig. 29

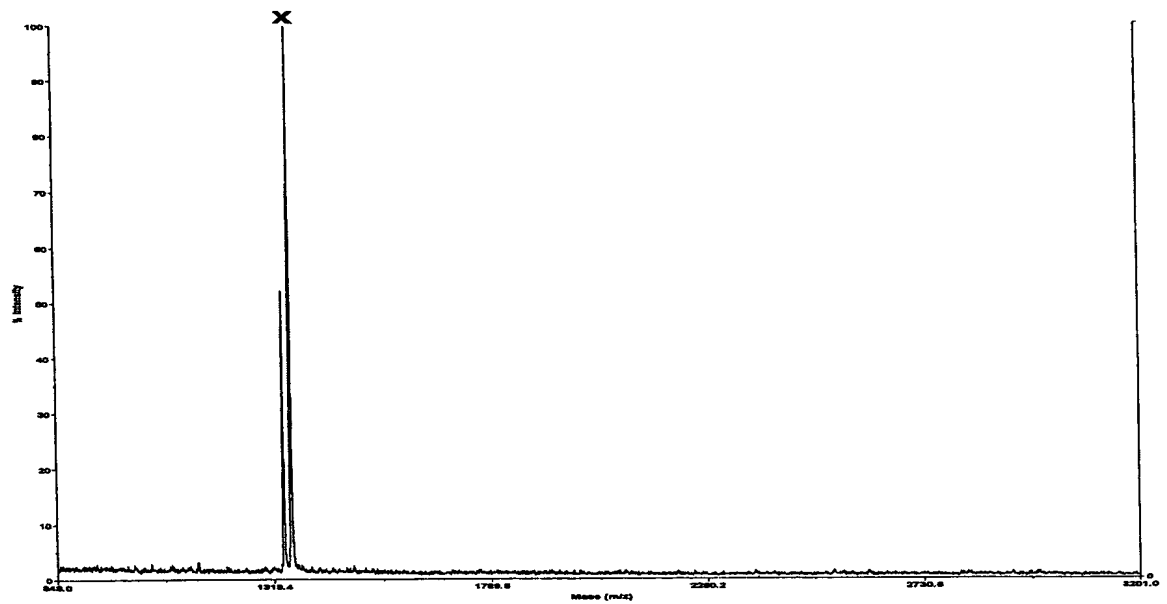


Fig. 30

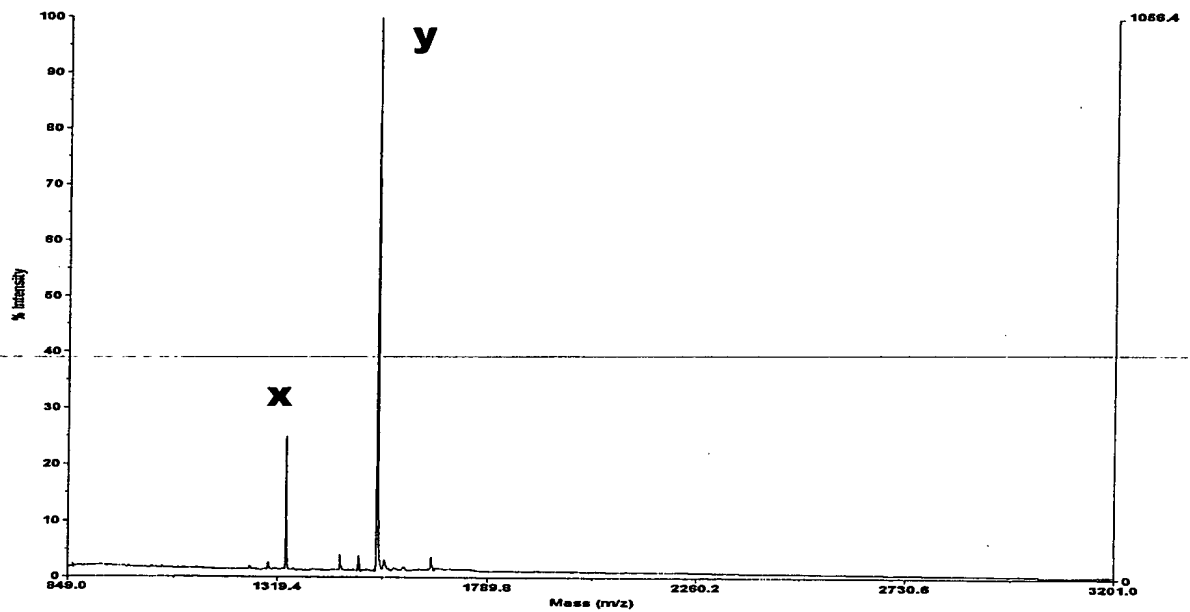


Fig. 31

Sheet 42 of 48

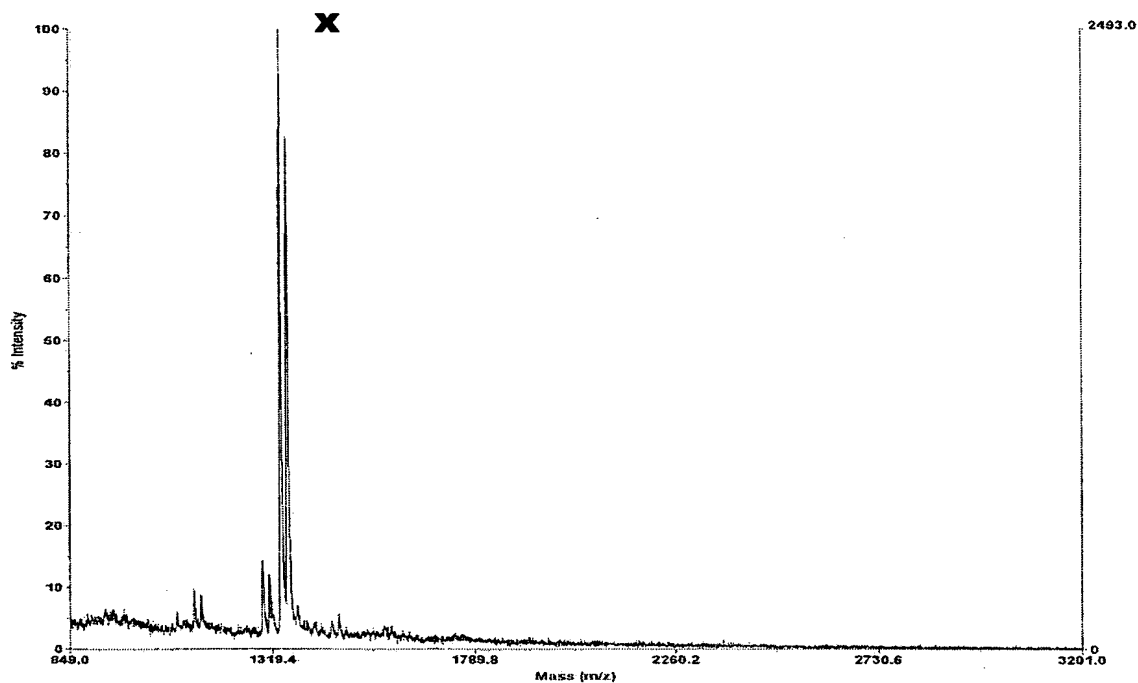
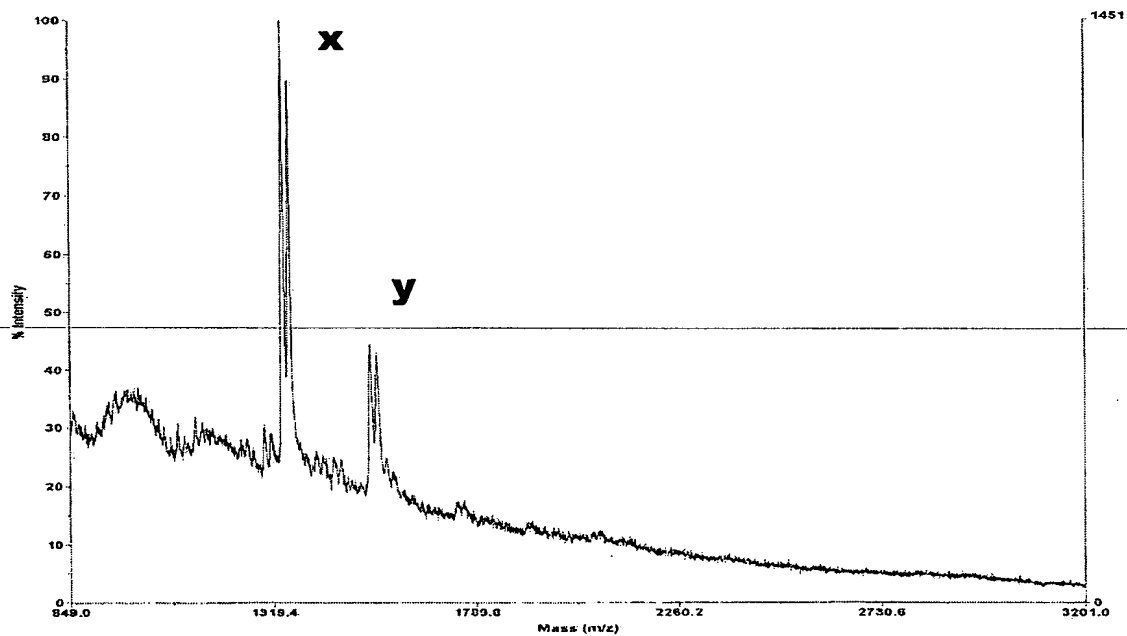


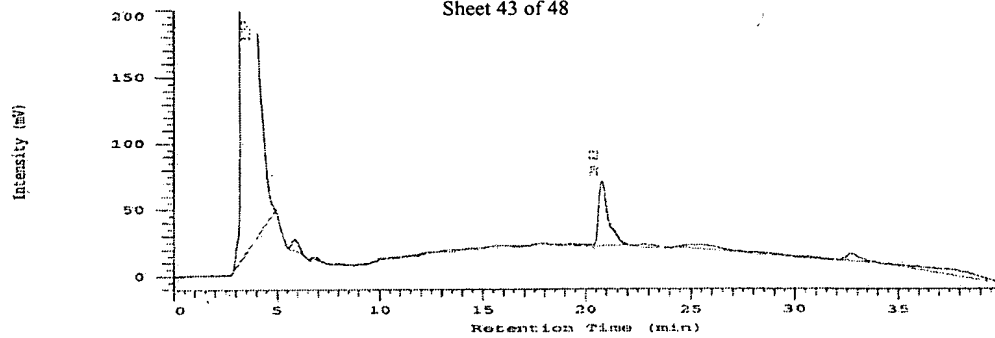
Fig. 32



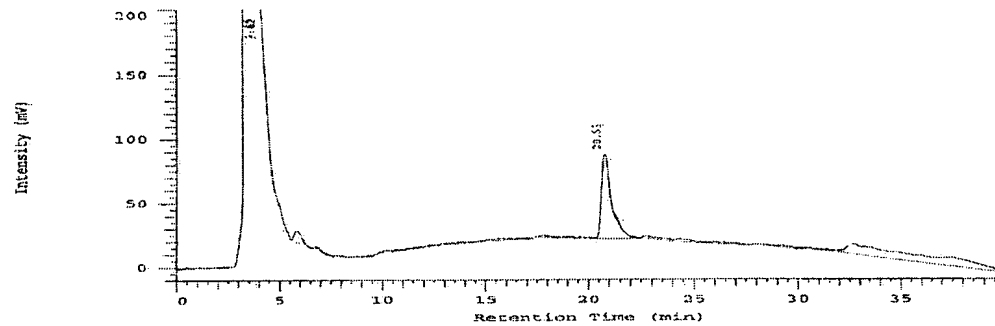
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Sheet 43 of 48

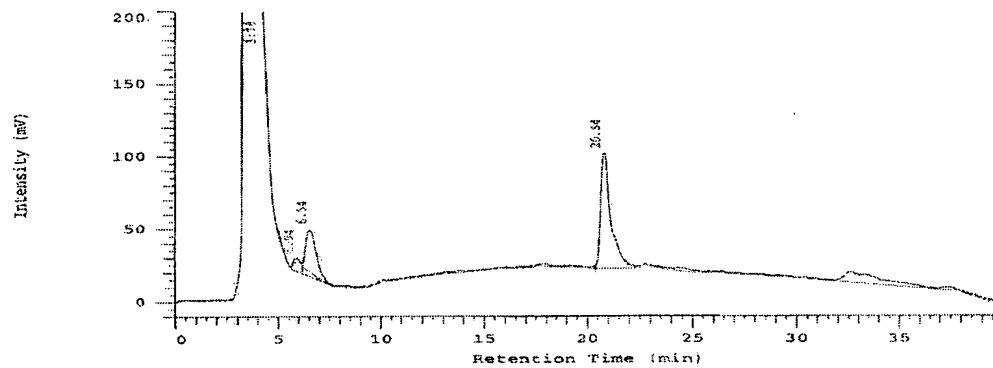
A



B



C



D

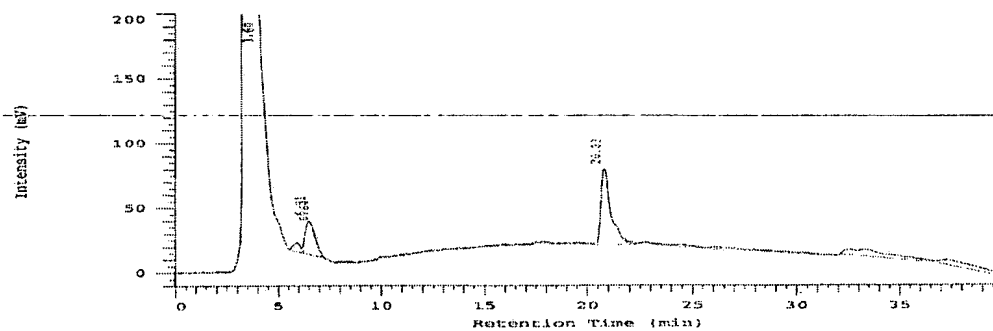
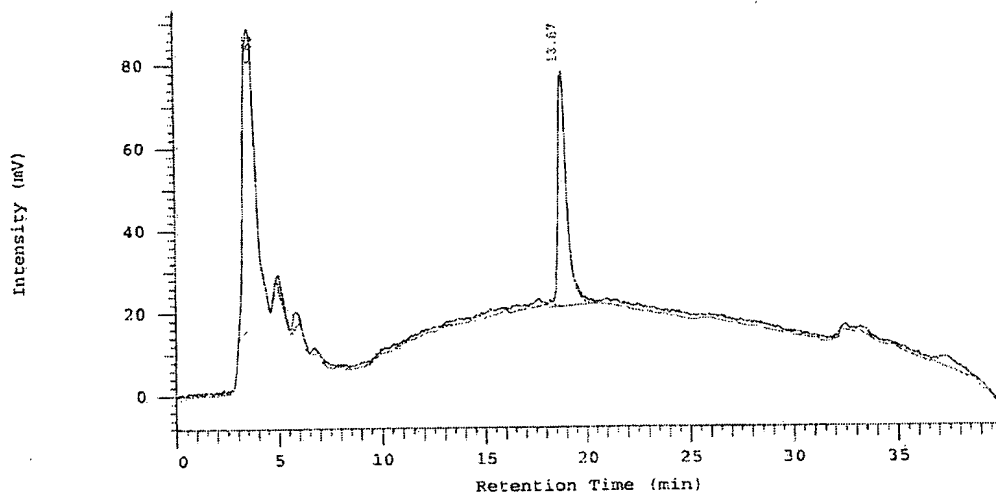


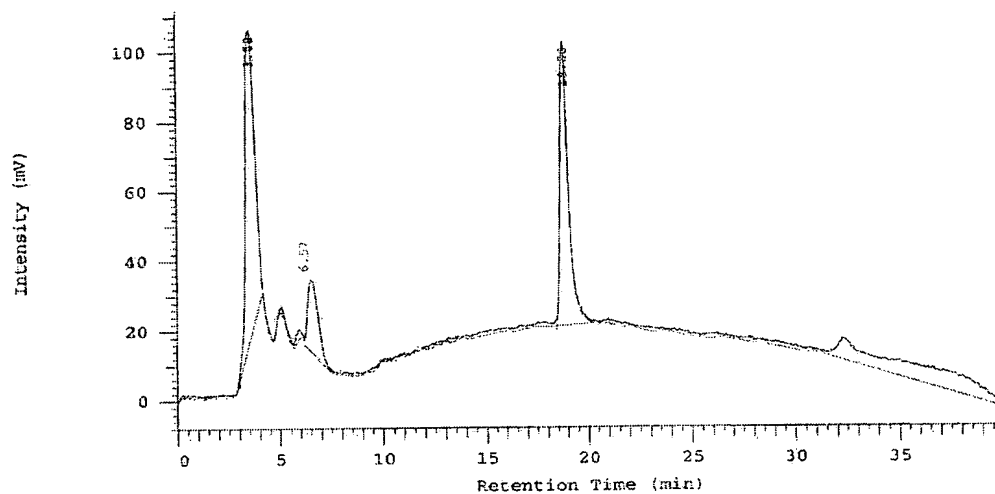
Fig. 33

Sheet 44 of 48

A



B



C

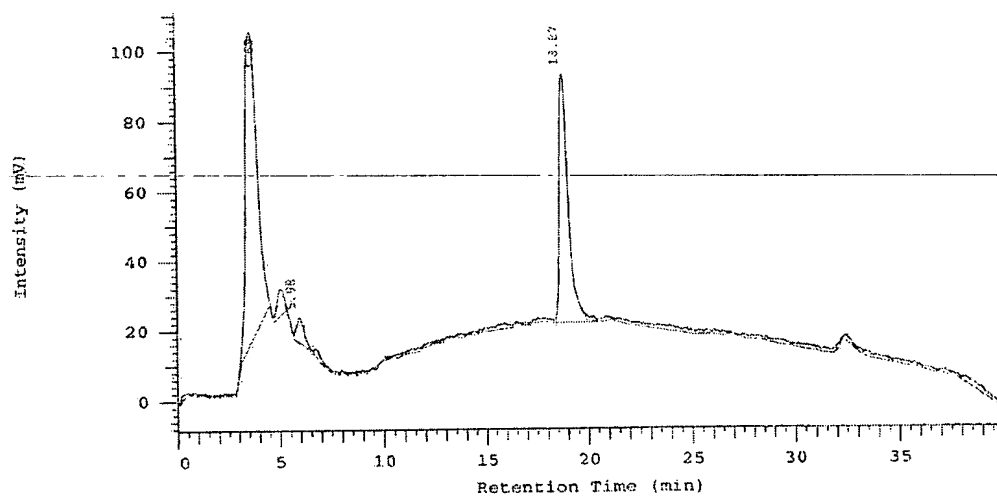


Fig. 34

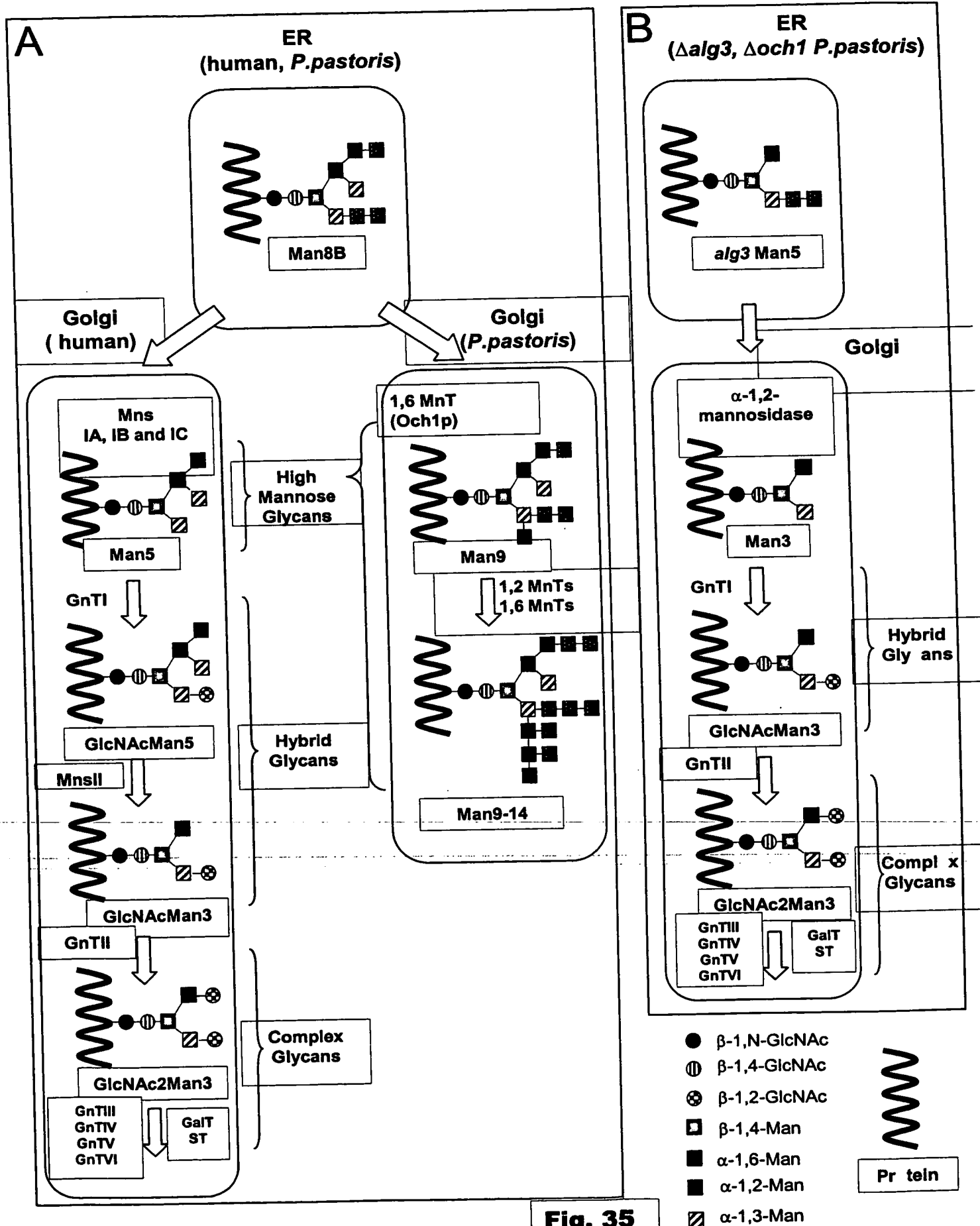


Fig. 36

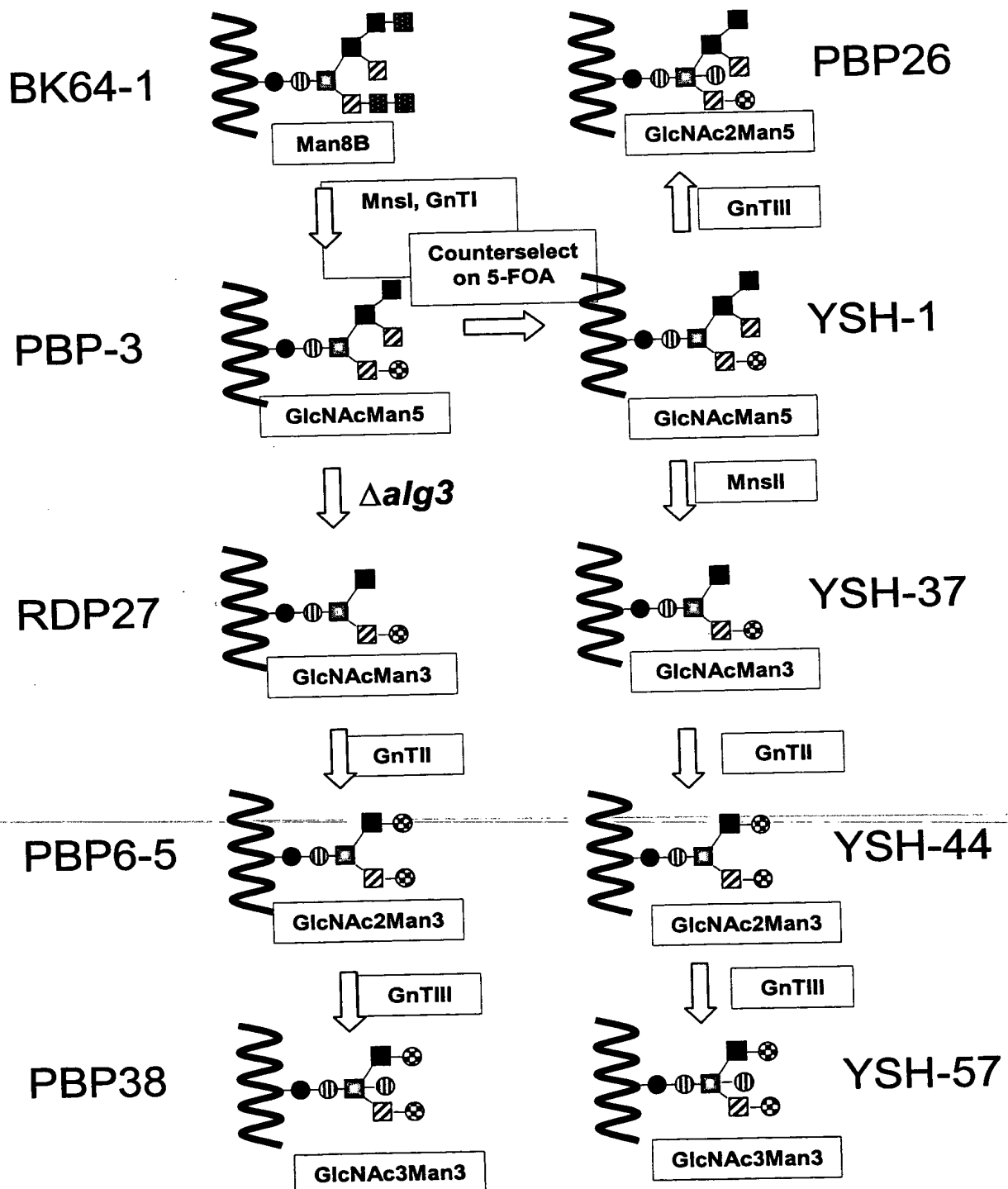


Fig. 37

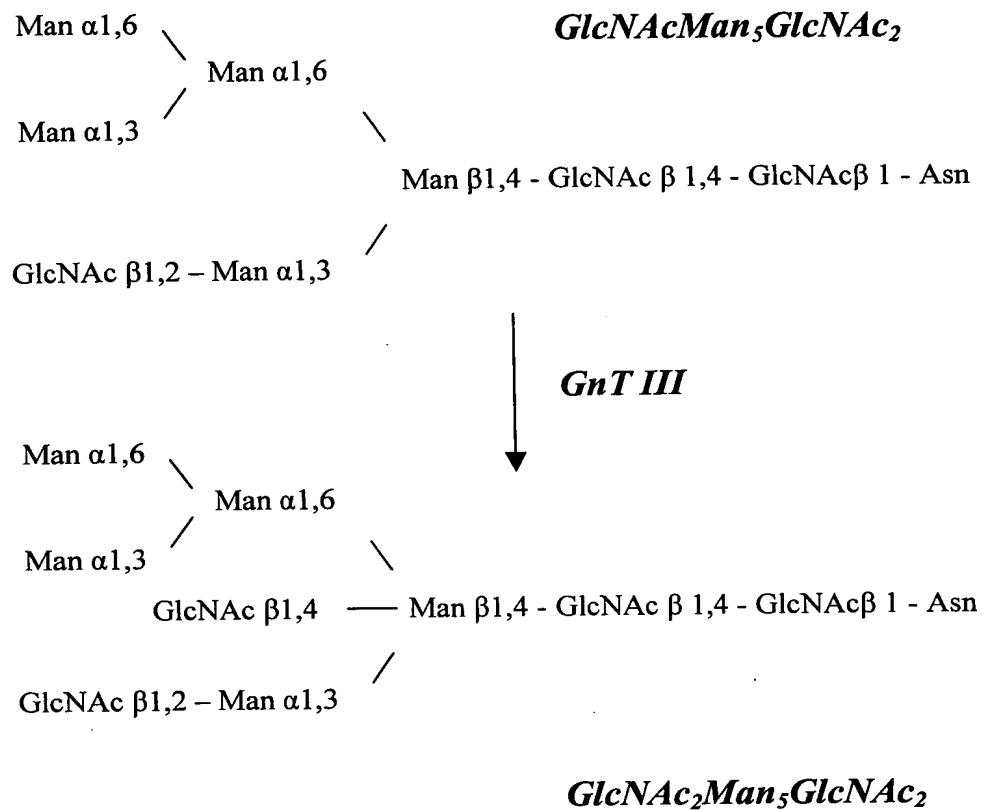


Fig. 38

